

Result No.	Score	Query Match	Length	DB ID	Description
1	1165	100.0	231	4	US-10-386-972-2 Sequence 2, Appli
2	1160	99.6	231	3	US-10-386-972-2 Sequence 2, Appli
3	1160	99.6	231	4	US-10-386-972-2 Sequence 2, Appli
4	423.5	36.4	265	1	US-07-958-551-2 Sequence 2, Appli
5	423.5	36.4	265	1	US-08-129-610-7 Sequence 7, Appli
6	423.5	36.4	265	1	US-08-129-610-7 Sequence 7, Appli
7	423.5	36.4	265	1	US-08-129-610-7 Sequence 7, Appli
8	423.5	36.4	265	1	US-08-129-610-7 Sequence 7, Appli
9	423.5	36.4	265	2	US-08-657-579A-2 Sequence 7, Appli
10	423.5	36.4	265	3	US-09-224-025-7 Sequence 7, Appli
11	423.5	36.4	265	4	US-09-706-541-7 Sequence 7, Appli
12	423.5	36.4	265	5	PCT-US94-07887-7 Sequence 7, Appli
13	417	35.8	222	1	US-08-129-610-8 Sequence 8, Appli
14	417	35.8	222	1	US-08-129-60A-8 Sequence 8, Appli
15	417	35.8	222	1	US-08-455-313-7 Sequence 8, Appli
16	417	35.8	222	1	US-08-475-313-8 Sequence 8, Appli
17	417	35.8	222	2	US-08-657-579A-3 Sequence 3, Appli
18	35.8	222	3	US-09-224-025-8 Sequence 8, Appli	
19	417	35.8	222	4	US-08-941-8 Sequence 8, Appli
20	417	35.8	222	5	PCT-US94-07887-8 Sequence 4, Appli
21	97	8.3	1833	4	US-08-621-94A-4 Sequence 4, Appli
22	97	8.3	1833	4	US-08-945-567D-4 Sequence 3, Appli
23	97	8.3	1992	4	US-08-621-94A-3 Sequence 3, Appli
24	97	8.3	1992	4	US-08-945-567D-3 Sequence 3, Appli
25	97	8.3	2048	3	US-08-268-347-48 Sequence 48, Appli
26	93	8.0	2123	3	US-08-948-68A-10 Sequence 10, Appli
27	89.5	7.7	624	4	US-09-248-796A-24363 Sequence 24363, A

Patent No. 6093695  
 GENERAL INFORMATION:  
 APPLICANT: Rupar, Mark J.  
 APPLICANT: Donovan, William P.  
 APPLICANT: Tan, Yiping  
 APPLICANT: Slaney, Annette C.  
 TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYET29  
 TITLE OF INVENTION: COMPOSITIONS TOXIC TO COLEOPTERAN  
 TITLE OF INVENTION: INSECTS AND CTENOCEPHALIDES spp.  
 NUMBER OF SEQUENCES: 4  
 COMPUTER READABLE FORM:  
 COMPUTER: IBM PC compatible  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION NUMBER: US/08/721,259  
 APPLICATION NUMBER: US/08/721,259  
 FILING DATE: Concurrently Herewith  
 CLASSIFICATION: 800  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Kitchell, Barbara S.  
 REGISTRATION NUMBER: 33,928  
 REFERENCE/DOCKET NUMBER: MOBT:017  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (512) 418-3000  
 TELEFAX: (512) 474-7577  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 231 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-721-259-2

Query Match 99.6%; Score 1160; DB 3; Length 231;  
 Best Local Similarity 99.6%; Pred. No. 8.6e-111;  
 Matches 230; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MFENRVTITLTVSSDVYNSSEIYQAPQYNNQALTLAKYFQGAIDGSTLRFDEKALQIA 60  
 Db 1 MFENRVTITLTVSSDVYNSSEIYQAPQYNNQALTLAKYFQGAIDGSTLRFDEKALQIA 60  
 Qy 61 NDIPQAQAVNTLNQTVQGTQVSYNIDKIVDIMKNVLSTVDNKKFWDQVTAATNTFT 120  
 Db 61 NDIPQAQAVNTLNQTVQGTQVSYNIDKIVDIMKNVLSTVDNKKFWDQVTAATNTFT 120  
 Qy 121 NLNSQESEAWIIFYKEDAKHTSYYNNLFAIQDEETGGMAMTLPADISVDEKEKVLF 180  
 Db 121 NLNSQESEAWIIFYKEDAKHTSYYNNLFAIQDEETGGMAMTLPADISVDEKEKVLF 180  
 Qy 181 VTIKDTEINYATVKAINVQALQSSRSKVDAFSPRLPRKRKICNS 231  
 Db 181 VTIKDTEINYATVKAINVQALQSSRSKVDAFSPRLPRKRKICNS 231  
 Qy 181 VTIKDTEINYATVKAINVQALQSSRSKVDAFSPRLPRKRKICNS 231  
 Db 181 VTIKDTEINYATVKAINVQALQSSRSKVDAFSPRLPRKRKICNS 231

RESULT 4  
 US-09-611-216-2  
 Sequence 2, Application US/09611216  
 Patent No. 6337756  
 GENERAL INFORMATION:  
 APPLICANT: Rupar, Mark J.  
 APPLICANT: Donovan, William P.  
 APPLICANT: Tan, Yiping  
 APPLICANT: Slaney, Annette C.  
 TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYET29  
 TITLE OF INVENTION: COMPOSITIONS TOXIC TO COLEOPTERAN

TITLE OF INVENTION: INSECTS AND CTENOCEPHALIDES spp.  
 NUMBER OF SEQUENCES: 4  
 COMPUTER READABLE FORM:  
 COMPUTER: Arnold, White & Durkee  
 ADDRESS: P. O. Box 4433  
 CITY: Houston  
 STATE: Texas  
 COUNTRY: United States of America  
 ZIP: 77210  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC Compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/611,216  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/721,259  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Kitchell, Barbara S.  
 REGISTRATION NUMBER: 33,928  
 REFERENCE/DOCKET NUMBER: MOBT:017  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (512) 418-3000  
 TELEFAX: (512) 474-7577  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 231 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-611-216-2

Query Match 99.6%; Score 1160; DB 4; Length 231;  
 Best Local Similarity 99.6%; Pred. No. 8.6e-111;  
 Matches 230; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MFFNRVTITLTVSSDVYNSSEIYQAPQYNNQALTLAKYFQGAIDGSTLRFDEKALQIA 60  
 Db 1 MFFNRVTITLTVSSDVYNSSEIYQAPQYNNQALTLAKYFQGAIDGSTLRFDEKALQIA 60  
 Qy 61 NDIPQAQAVNTLNQTVQGTQVSYNIDKIVDIMKNVLSTVDNKKFWDQVTAATNTFT 120  
 Db 61 NDIPQAQAVNTLNQTVQGTQVSYNIDKIVDIMKNVLSTVDNKKFWDQVTAATNTFT 120  
 Qy 121 NLNSQESEAWIIFYKEDAKHTSYYNNLFAIQDEETGGMAMTLPADISVDEKEKVLF 180  
 Db 121 NLNSQESEAWIIFYKEDAKHTSYYNNLFAIQDEETGGMAMTLPADISVDEKEKVLF 180  
 Qy 181 VTIKDTEINYATVKAINVQALQSSRSKVDAFSPRLPRKRKICNS 231  
 Db 181 VTIKDTEINYATVKAINVQALQSSRSKVDAFSPRLPRKRKICNS 231

RESULT 4  
 US-09-598-551-2  
 Sequence 2, Application US/07958551  
 Patent No. 5302387  
 GENERAL INFORMATION:  
 APPLICANT: Payne, Jewel M.  
 APPLICANT: Kennedy, Keith M.  
 APPLICANT: Randall, John Brooks  
 APPLICANT: Brower, David Orin  
 TITLE OF INVENTION: Bacillus thuringiensis Isolates Active Against Cockroaches and Genes Encoding Cockroach-Active Toxins  
 NUMBER OF SEQUENCES: 2  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: David R. Saliwanchik  
 STREET: 2421 N.W. 41st Street, Suite A-1

CITY: Gainesville  
 STATE: FL  
 COUNTRY: USA  
 ZIP: 32606  
 COMPUTER READABLE FORM:  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 PILING NUMBER: US/07/958,551  
 PILING DATE: October 19, 1992  
 CLASSIFICATION: 424  
 PRIOR APPLICATION DATA:  
 PRIORITY NUMBER: 07/788,654  
 PILING DATE: No. 5302387ember 6, 1991

ATTORNEY/AGENT INFORMATION:  
 NAME: Saliwanchik, David R.  
 REGISTRATION NUMBER: 31,794  
 REFERENCE/DOCKET NUMBER: M/J 101.C2  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 904-375-8100  
 TELEFAX: 904-372-5800  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 HYPOTHETICAL: YES  
 LENGTH: 265 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: *Bacillus thuringiensis*  
 STRAIN: neoleogenes  
 INDIVIDUAL ISOLATE: PS201T6  
 IMMEDIATE SOURCE:  
 LIBRARY: LambdaGem (TM)-11 Library of Kenneth B.  
 CLONE: 201T635

-07-958-551-2

Query Match 36.4% Score 423.5; DB 1; Len 40.9%; Pred. No. 3e-35; Mismatches 72; In

5	RVITLTVPSSPDVNNYSEIYQVA-	-	-	PQYINQALATLAKYFGQA
38	RVITYLKV--KDPDTTQOLLETBIEENENYVQIAQLAAAFQDAA			
55	KALQIANDI-PQAVAVNTLNQTVQQGTIVQVSIMIDKIVDMMKN			
96	KGLEVAKTIQPKGAVAYTDQTLSQSINNOVSIMIDRVISVLKT			
114	AITNTFTNLSOSEANANTYKDAHTKTSYYNNILFAIQDDETT			
155	ATDDTFNTLNQTDNSAVFWGETSHQNTNYVNMPAIQNNTT			
174	EKRKVLFVTTIKOTENYVATVKAINVYQALQSSRSKVD--A			
215	DICRTVFLPTTDXYANTSVNQIQLRFAQPLTDARSALNSINDLSEA			

RESULT 5  
 -08-129-610-7  
 Sequence 7, Application US/08129610  
 Patent No. 5436002  
 GENERAL INFORMATION:  
 APPLICANT: Jewel Payne  
 APPLICANT: Kenneth Narva  
 APPLICANT: Kendrick Akira Uyeda  
 APPLICANT: Christine Julie Stalder  
 APPLICANT: Tracy Ellis Michaela

TITLE OF INVENTION: No. 5436002e1 Bacillus thuringiensis Isolates and Toxins  
 NUMBER OF SEQUENCES: 10  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: David R. Saliwanchik  
 STREET: 2421 N.W. 41st Street, Suite A-1  
 CITY: Gainesville  
 STATE: FL  
 COUNTRY: USA  
 ZIP: 32606  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/129,610  
 FILING DATE:  
 CLASSIFICATION: 800  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/093,199  
 FILING DATE: 15-JUL-1993  
 NAME:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/977,350  
 FILING DATE: 17-NOV-1992  
 NAME:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07//746,751  
 FILING DATE: 21-AUG-1991  
 NAME:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07//708,266  
 FILING DATE: 28-MAY-1991  
 NAME:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07//647,399  
 FILING DATE: 29-JAN-1991  
 NAME:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Saliwanchik, David R.  
 REGISTRATION NUMBER: 31,794  
 REFERENCE/DOCKET NUMBER: MA55CCD.C1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 904-375-8100  
 TELEFAX: 904-372-5800  
 INFORMATION FOR SEQ ID NO: 7:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 265 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: Single  
 TOPOLOGY: Linear  
 MOLECULE TYPE: Protein  
 HYPOTHETICAL: YES  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Bacillus thuringiensis  
 STRAIN: neoleoensis  
 INDIVIDUAL ISOLATE: PS201T6  
 IMMEDIATE SOURCE:  
 LIBRARY: LambdaGem (TM)-11 Library of Kenneth E. Narva  
 CLONE: 201T635  
 US-08-129-610-7

Query Match Score 423 5; DB 1; Length 265;  
 Best Local Similarity 40.9%; Pred. No. 3e-35'; Mismatches 72'; Indels 17; Gaps 6;  
 Matches 94 ; Conserv. 47 ;

Qy 5 RVITLTVPSDVNVYSEIYQVA---POTYNQALTIKAYFGQAI----DGSTLRFDE 54  
 Db 38 RVIYLVK--KDPIDDTTOLLETTIENPNVYQAIQLAFAAFDALVPTETEGBAIRPSMP 95  
 Qy 55 KALQIANDI-PQAAVNTINQTVGCTVQSVMDIKVDMANVLISIVDNKFWDDVTA 113

Db 96 KGLEVAKTIQPKGAVVAYTDQTLQSNNQVSYMDRVISVLUKTNGVALSG-SITOLTA 154  
 Qy 114 AITNTFTNINSQSESEWIFIYKEDAHKTTYYXNLLFRAIQDEBTGUMATLPIAFDISVDI 173  
 Db 155 AITDTFTNLNTQDSAWFWGKETSHQTNTYNNMPAIQNETTGRVMCMCPIGPEIRVFT 214  
 Qy 174 EKEKVLFPTIKDENTAVTKAIVNVQALQSSRSKVD--AFPSPRHL 220  
 Db 215 DKRTVLFPTTDYANXSVNIQTLRFQPLDSRALSINDLSERASSKYL 264

RESULT 6  
 US-08-129-609A-7  
 ; Sequence 7, Application US/08129609A  
 ; General Information:  
 ; Patent No. 5635432  
 ; APPLICANT: Jewel Payne  
 ; APPLICANT: M. Keith Kennedy  
 ; APPLICANT: John Brookes Randal  
 ; APPLICANT: H. Ernest Schneper  
 ; TITLE OF INVENTION: Bacillus thuringiensis Isolates Active Toxins  
 ; NUMBER OF SEQUENCES: 10  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: David R. Saliwanchik  
 ; STREET: 2421 N.W. 41st Street, Suite A-1  
 ; CITY: Gainesville  
 ; STATE: FL  
 ; COUNTRY: USA  
 ; ZIP: 32606  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/129,609A  
 ; FILING DATE: 30-SEP-1993  
 ; CLASSIFICATION: 435  
 ; PRIORITY APPLICATION DATA:  
 ; APPLICATION NUMBER: 07/958,551  
 ; FILING DATE: 19-OCT-1992  
 ; PRIORITY APPLICATION DATA:  
 ; APPLICATION NUMBER: 07/88,654  
 ; FILING DATE: 6-NOV-1991  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Saliwanchik, David R.  
 ; REGISTRATION NUMBER: 31,794  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 904-375-8100  
 ; TELEFAX: 904-372-5800  
 ; INFORMATION FOR SEQ ID NO: 7:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 265 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; HYPOTHETICAL: YES  
 ; ANTI-SENSE: NO  
 ; ORIGINAL SOURCE:  
 ; ORGANISM: Bacillus thuringiensis  
 ; STRAIN: neleensis  
 ; INDIVIDUAL ISOLATE: PS201T6  
 ; IMMEDIATE SOURCE:  
 ; LIBRARY: LambdaGem (TM) -11 Library of Kenneth E. Narva  
 ; CLONE: 201T635

Db 94 Conservative 47; Mismatches 72; Indels 17; Gaps 6;  
 Qy 5 RVIITLYPSSDVNVYSEIYQVA---POXINGALILAKYFOGAI-----DGSTLFRDFE 54  
 Db 38 RVYLVY--KDPIDTQOLITEINPNPYLQAOIOLAATQDALVYPTETEFGEARFSMP 95  
 Qy 55 KALQZANDI-PQAAVNTLNQTVQGSTQVSVMIDKVIDLMNVTUSIVIDNKKFDQVTA 113  
 Db 96 KGLEVAKTIQPKGAVVAYTDQTLSSRNQSYWMIRVISVLUKTNGVALSG-SITOLTA 154  
 Qy 114 ATTTFTNLSQESAWIIFYKEDAHKTSYNTLFAIQDEBTGUMATLPIAFDISVDI 173  
 Db 155 ATTTFTNLTQDSAWFWGKETSHQTNTYNNMPAIQNETTGRVMCMCPIGPEIRVFT 214  
 Qy 174 EKEKVLFPTIKDENTAVTKAIVNVQALQSSRSKVD--AFPSPRHL 220  
 Db 215 DKRTVLFPTTDYANXSVNIQTLRFQPLDSRALSINDLSERASSKYL 264

RESULT 7  
 US-08-455-313-7  
 ; Sequence 7, Application US/08455313  
 ; Patent No. 5635430  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Jewel Payne  
 ; APPLICANT: Kenneth Narva  
 ; APPLICANT: Kendrick Akira Iyeda  
 ; APPLICANT: Christine Julie Stalder  
 ; APPLICANT: Tracy Ellis Michaels  
 ; TITLE OF INVENTION: No. 5635480e1. Bacillus thuringiensis Isolates and Toxins  
 ; NUMBER OF SEQUENCES: 10  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: David R. Saliwanchik  
 ; STREET: 2421 N.W. 41st Street, Suite A-1  
 ; CITY: Gainesville  
 ; STATE: FL  
 ; COUNTRY: USA  
 ; ZIP: 32606  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/455,313  
 ; FILING DATE: 31-MAY-1995  
 ; CLASSIFICATION: 514  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/129,610  
 ; FILING DATE: 30-SEP-1993  
 ; APPLICATION NUMBER: US/08/093,199  
 ; FILING DATE: 15-JUL-1993  
 ; CLASSIFICATION: 514  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/07/977,350  
 ; FILING DATE: 17-NOV-1992  
 ; CLASSIFICATION: 514  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/708,266  
 ; FILING DATE: 28-MAY-1991  
 ; CLASSIFICATION: 514  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/647,399  
 ; FILING DATE: 29-JAN-1991  
 ; CLASSIFICATION: 514  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/746,751  
 ; FILING DATE: 21-AUG-1991  
 ; CLASSIFICATION: 514  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/977,350  
 ; FILING DATE: 17-NOV-1992  
 ; CLASSIFICATION: 514  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/746,751  
 ; FILING DATE: 21-AUG-1991  
 ; CLASSIFICATION: 514  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/647,399  
 ; FILING DATE: 29-JAN-1991  
 ; CLASSIFICATION: 514  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Saliwanchik, David R.  
 ; REGISTRATION NUMBER: 31,794  
 ; IMMEDIATE SOURCE:  
 ; LIBRARY: LambdaGem (TM) -11 Library of Kenneth E. Narva  
 ; CLONE: 201T635

Query Match Similarity 36.4%; Score 423.5; DB 1; Length 265;  
 Best Local Similarity 40.9%; Pred. No. 3e-35;

## TELECOMMUNICATION INFORMATION:

TELEPHONE: 904-375-8100

TELEFAX: 904-372-5800

SEQUENCE CHARACTERISTICS:

LENGTH: 265 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: YES

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: *Bacillus thuringiensis*STRAIN: *neoleoensis*

INDIVIDUAL ISOLATE: PS201T6

IMMEDIATE SOURCE:

LIBRARY: LambdaGem (TM)-11 Library of Kenneth E. Narva

CLONE: 201T635

US-08-455-313-7

Query Match Score 423.5%; DB 1; Length 265;  
Best Local Similarity 40.9%; Pred. No. 3e-35; Gaps 6;  
Matches 94; Conservative 47; Mismatches 72; Indels 17; Gaps 6;

Qy 5 RVIITLPPSSDVNYSRIVYQA---PQYNNQALTLAKYFGQAI---DGSTLRFDFE 54

Db 38 RVIYLKV--KDPIDTQLLETEIENPNVYLOQIAQLAAAFQDALVPTETEGAEIRFSMP 95

Qy 55 KALQIANDI--POAAYVNTLNQTVQOGTVOVSVMIDKIVDINKNVLSIVIDNKKFWQDTA 113

Db 96 KGLEVAKTIQPGKAVVAYTDQTLSQSNQSVWMDRVSLVLTGVALSG-SIIQTQTA 154

Qy 114 AITNTFTNLNSQEAWIIFYKEDAKTSYYNNLRAIQDEETGGUMATLPIAFD1SYDI 173

Db 155 AITDTFTNLNTQKDSAWFPNGKETSHQTNTYNVMPAIQNETTGRYMMCVPIGFELRVFT 214

Qy 174 BKEKVLFVTIKDENTAVTKAINVVOAQLQSSRDSKVVD--AFKSPRHL 220

Db 215 DKRTVLFITKDYANTSVNIQTLRFAQPLIDSRLSALSINDLSEALRSSKYL 264

RESULT 8  
US-08-475-924-2  
Sequence 2, Application US/08475924  
Patent No. 5723440  
GENERAL INFORMATION:  
APPLICANT: Stockhoff, Brian  
APPLICANT: Conlan, Christopher  
TITLE OF INVENTION: CONTROLLING HEMIPTERAN INSECT PESTS  
TITLE OF INVENTION: WITH *BACILLUS THURINGIENSIS*  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: David R. Saliwanchik  
STREET: 2421 N.W. 41st Street, Suite A-1  
CITY: Gainesville  
STATE: FL  
COUNTRY: USA  
ZIP: 32606COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/657,579A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Saliwanchik, David R.  
REGISTRATION NUMBER: 31,794  
REFERENCE/DOCKET NUMBER: NA96  
TELECOMMUNICATION INFORMATION:RESULT 9  
US-08-657-579A-2  
Sequence 2, Application US/08657579A  
Patent No. 5885963  
GENERAL INFORMATION:  
APPLICANT: Stockhoff, Brian  
APPLICANT: Conlan, Christopher  
TITLE OF INVENTION: CONTROLLING HEMIPTERAN INSECT PESTS  
TITLE OF INVENTION: WITH *BACILLUS THURINGIENSIS*  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Saliwanchik & Saliwanchik  
STREET: 2421 N.W. 41st Street, Suite A-1  
CITY: Gainesville  
STATE: FL  
COUNTRY: USA  
ZIP: 32606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/657,579A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Sanders, Jay M.

REGISTRATION NUMBER: 39,355  
 REFERENCE/DOCKET NUMBER: MA96.C1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 352-315-8100  
 TELEFAX: 352-372-5800  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 265 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 HYPOTHETICAL: YES  
 ANTI SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: *Bacillus thuringiensis*  
 SPAIN: neoleonensis  
 INDIVIDUAL ISOLATE: PS201T6  
 IMMEDIATE SOURCE:  
 LITERARY: LambdaGem (TM) -11 Library of Kenneth E. Narva  
 CLONE: 2011635  
 US-08-657-579A-2

Query Match 36.4%; Score 423.5; DB 2; Length 265;  
 Best Local Similarity 40.9%; Pred. No. 3e-35; Gaps 6;  
 Matches 94; Conservative 47; Mismatches 72; Indels 17;

Qy 5 RVIITLTVPSSDVVNYSEIYQVA---PQQYNQALTAIAYKFGAI----DGSTARDFDE 54  
 .Db 38 RVIYLVY--KDPIDTQLLETEIENPVYQAIQLAATQDALVPTETEFGEARFSMP 95

Qy 55 KALQIANDI-PQAAVINTLNQTYQOGTVQSYVMIDKIVDIMKNVLISIVLDNKKFMDQVTA 113  
 Db 96 KGLEVAKTIOQGAVVAYTDQTLSQNNQVSVMDRVSLTKTNGVALSG-STITQLTA 154

Qy 114 AITNTTPNLNSQESEAWTFQKEDAHKTSTYYNNLPAIDDEETGGYMATPIAFDIDSVDI 173  
 Db 155 AITDTPFLNLTQKDSAWFWKGSKETSHQTQNTYNNMFAIONNETTGRYMMCPIGGFELRVFT 214

Qy 174 EKEKVLFVTTKDENTAVTAKVNVQALQSSRSKVD--AFKSPrHL 220  
 Db 215 DKRTVLFLLTDXYANYSVNQIQTFLRFAQPLIDSRLSINDLSBEALKSSKYL 264

RESULT 10  
 US-09-224-025-7  
 Sequence 7, Application US/09224025  
 Paten No. 6150165  
 GENERAL INFORMATION:  
 APPLICANT: Jewel Payne  
 APPLICANT: Kenneth Narva  
 APPLICANT: Kendrick Akira Ueda  
 APPLICANT: Christine Julie Strader  
 APPLICANT: Tracy Ellis Michael  
 TITLE OF INVENTION: No. 6150165el *Bacillus thuringiensis* Isolates and Toxins  
 NUMBER OF SEQUENCES: 10  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEES: David R. Salivanchik  
 STREET: 2421 N.W. 41st Street, Suite A-1  
 CITY: Gainesville  
 STATE: FL  
 COUNTRY: USA  
 ZIP: 32606  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC Compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/224, 025  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/455,313  
 FILING DATE: 08/09/93, 199  
 APPLICATION NUMBER: US 08/093,199  
 FILING DATE: 15-JUL-1993  
 CLASSIFICATION:  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 07/977,350  
 FILING DATE: 17-NOV-1992  
 CLASSIFICATION:  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 07/746,751  
 FILING DATE: 21-AUG-1991  
 CLASSIFICATION:  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 07/708,266  
 FILING DATE: 28-MAY-1991  
 CLASSIFICATION:  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 07/647,399  
 FILING DATE: 29-JAN-1991  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Salivanchik, David R.  
 REGISTRATION NUMBER: 31,794  
 REFERENCE/DOCKET NUMBER: MA55CCD.C1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 904-375-8100  
 TELEFAX: 904-371-5800  
 INFORMATION FOR SEQ ID NO: 7:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 265 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 HYPOTHETICAL: YES  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: *Bacillus thuringiensis*  
 STRAIN: neoleonensis  
 INDIVIDUAL ISOLATE: PS201T6  
 IMMEDIATE SOURCE:  
 LIBRARY: LambdaGem (TM)-11 Library of Kenneth E. Narva  
 CLONE: 2011635

US-09-224-025-7

Query Match 36.4%; Score 423.5; DB 3; Length 265;  
 Best Local Similarity 40.9%; Pred. No. 3e-35; Gaps 6;  
 Matches 94; Conservative 47; Mismatches 72; Indels 17;

Qy 5 RVIITTVPSDVVNYSEIYQVA---PQINQALIYKFGAI----DGSTARDFDE 54  
 .Db 38 RVIYLVY--KDPIDTQLLETEIENPVYQAIQLAATQDALVPTETEFGEARFSMP 95

Qy 55 KALQIANDI-PQAAVINTLNQTYQOGTVQSYVMIDKIVDIMKNVLISIVLDNKKFMDQVTA 113  
 Db 96 KGLEVAKTIOQGAVVAYTDQTLSQNNQVSVMDRVSLTKTNGVALSG-STITQLTA 154

Qy 114 AITNTTPNLNSQESEAWTFQKEDAHKTSTYYNNLPAIDDEETGGYMATPIAFDIDSVDI 173  
 Db 155 AITDTPFLNLTQKDSAWFWKGSKETSHQTQNTYNNMFAIONNETTGRYMMCPIGGFELRVFT 214

Qy 174 EKEKVLFVTTKDENTAVTAKVNVQALQSSRSKVD--AFKSPrHL 220  
 Db 215 DKRTVLFLLTDXYANYSVNQIQTFLRFAQPLIDSRLSINDLSBEALKSSKYL 264

RESULT 11  
 US-09-706-541-7  
 Sequence 7, Application US/09706541  
 Paten No. 6689743  
 GENERAL INFORMATION:  
 APPLICANT: Jewel Payne

Kenneth B. Narva  
 Kendrick A. Uyeda  
 Christine J. Staider  
 Tracy E. Michaels  
 Bacillus thuringiensis Isolates and Toxins  
 NUMBER OF SEQUENCES: 10  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Jay M. Sanders  
 STREET: 2421 N.W. 41st Street, Suite A-1  
 CITY: Gainesville  
 STATE: FL  
 COUNTRY: USA  
 ZIP: 32606  
 COMPUTER READABLE FORM:  
 COMPUTER TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/706,541  
 FILING DATE: 03 -NO- 6689743-2000  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 09/224,025  
 FILING DATE: 31-DEC-1998  
 APPLICATION NUMBER: US 08/770,933  
 FILING DATE: 20-DEC-1996  
 APPLICATION NUMBER: US 08/455,313  
 FILING DATE: 31-MAY-1995  
 APPLICATION NUMBER: US 08/129,610  
 FILING DATE: 30-SEP-1993  
 APPLICATION NUMBER: US 08/093,199  
 FILING DATE: 15-JUL-1993  
 APPLICATION NUMBER: US 07/977,350  
 FILING DATE: 17-NOV-1992  
 APPLICATION NUMBER: US 07/746,751  
 FILING DATE: 21-AUG-1991  
 APPLICATION NUMBER: US 07/708,266  
 FILING DATE: 05-MAY-1991  
 APPLICATION NUMBER: US 07/647,399  
 FILING DATE: 29-JAN-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Sanders, Jay M.  
 REGISTRATION NUMBER: 39,355  
 REFERENCE/DOCKET NUMBER: MA-55CCDCD4  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 352-375-8100  
 TELEFAX: 352-372-5800  
 INFORMATION FOR SEQ ID NO: 7:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 265 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 HYPOTHETICAL: YES  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Bacillus thuringiensis  
 STRAIN: neotobensis  
 INDIVIDUAL ISOLATE: PS201T6  
 IMMEDIATE SOURCE:  
 LIBRARY: LambdaGen (TM)-11 Library of Kenneth B. Narva  
 CLONE: 201T35  
 SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
 US-09-706-41-7

SEQUENCE CHARACTERISTICS:  
 LENGTH: 265 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 HYPOTHETICAL: YES  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: *Bacillus thuringiensis*  
 STRAIN: neoleoensis  
 CLONE: PS20176  
 INDIVIDUAL ISOLATE: PS20176  
 IMMEDIATE SOURCE: LambdaGen (TM) -11 Library of Kenneth E. Narva  
 LIBRARY: LambdaGen (TM) -11 Library of Kenneth E. Narva  
 CLONE: PS20176  
 PCT-US94-07897-7

Query Match Score 423.5; DB 5; Length 265;  
 Best Local Similarity 40.9%; Pred. No. 3e-35; Gaps 6;  
 Matches 94; Conservative 47; Mismatches 72; Indels 17; Gaps 6;

Qy 5 RVIITVPPSDVVNVEIYQVA---POVNQALTLAKYFQGAI-----DGSTLRFDFE 54  
 Db 38 RVIYIKV--RDPIDTQLLETEIENPNYIQLAAAFQDALVPTTEFGEARF SMP 95

Qy 55 KALQIANDI POAAYVNTLNQTVQGTQVQSVMDKIVDIMKNVLSIVIDNKKFWDQVTA 113  
 Db 96 KGLLEVAKTIVQKGAVVAYTQTQSLQSNNQVSVMDRVISVLTQKTVGVAISG-SLITQTA 154

Qy 114 AITNTFTNNSQEESEWTFYKEDAHRTSYNILFAQDDEBTGEVMAFLPIAFDISVDI 173  
 Db 155 AITDFFTNLNTQDSAWFNGKETSHOTNTYNTNMFAQNBTGRVMCMCPIGFEIRVPT 214

Qy 174 EKEKYLFTVTKDTENYATVYKAIVNQALLOSSRDKVVD--APKSPPHL 220  
 Db 215 DRRTVLFITKDYANYTSVNIQTLRFAQPLIDSRLSALINIDSEALRSKYL 264

RESULT 13  
 US-08-129-610-8  
 Sequence 8, Application US/08129610  
 Patent No. 5436002

GENERAL INFORMATION:  
 APPLICANT: Jewel Payne  
 APPLICANT: Kenneth Narva  
 APPLICANT: Kendrick Akira Uyeda  
 APPLICANT: Christine Julie Stalder  
 APPLICANT: Tracy Ellis Michaels  
 TITLE OF INVENTION: No. 5436002el *Bacillus thuringiensis* Isolates and Toxins  
 NUMBER OF SEQUENCES: 10  
 ADDRESSEE: David R. Saliwanchik  
 STREET: 2421 N.W. 41st Street, Suite A-1  
 CITY: Gainesville  
 STATE: FL USA  
 COUNTRY: USA  
 ZIP: 32606  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/129, 610  
 FILING DATE:  
 CLASSIFICATION: 800  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/977, 350  
 FILING DATE: 17-NOV-1992  
 NAME:  
 PRIORITY DATA:  
 APPLICATION NUMBER: US 07/746, 751  
 FILING DATE: 21-AUG-1991  
 NAME:  
 PRIORITY DATA:  
 APPLICATION NUMBER: US 07/708, 266  
 FILING DATE: 28-MAY-1991  
 NAME:  
 PRIORITY DATA:  
 APPLICATION NUMBER: US 07/647, 399  
 FILING DATE: 29-JAN-1991  
 NAME:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Saliwanchik, David R.  
 REGISTRATION NUMBER: 31,794  
 REFERENCE/DOCKET NUMBER: MASS5CCD.C1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 904-75-8100  
 TELEFAX: 904-372-5800  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 222 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 HYPOTHETICAL: YES  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: *Bacillus thuringiensis*  
 SPRAIN: neoleoensis  
 INDIVIDUAL ISOLATE: PS20176  
 US-08-129-610-8

Query Match Score 35.8%; DB 1; Length 222;  
 Best Local Similarity 41.9%; Pred. No. 1.e-34;  
 Matches 91; Conservative 42; Mismatches 72; Indels 12; Gaps 5

Qy 15 DVVNNTSEIYQVA-POVNQALTLAKYFQGAI-----DGSTLRFDFEKAQIANDI-PQA 66  
 Db 6 DTTQLEIETENPNYIQLAAAFQDALVPTTEFGEARF SMPKCLEVAKTQPKG 65

Qy 67 AVVNTLNQTYQGTQVQSVMDKIVDIMKNVLSIVIDNKKFWDQVTAITNTFLNSQE 126  
 Db 66 AVVATDQTLQSNNQVSVMDRVISVLTQKTVGVAISG-SLITQTAITDFTNNTQK 124

Qy 127 SEAWFPYKEDAHRTSYNILFAQDDEBTGEVMAFLPIAFDISVCIPLFKD 186  
 Db 125 DSAWTWFGKETSHOTNTYTNMFAQNBTGRVMCMCPIGFEIRVPTLKTDY 184

Qy 187 ENYAVTVAINVQALQSSRSKVD--APKSPPHL 220  
 Db 185 ANYSVNIQTRFAQQPLIDSRLSALINIDSEALRSKYL 221

RESULT 14  
 US-08-129-609A-8  
 Sequence 8, Application US/08129609A  
 Patent No. 5489432  
 GENERAL INFORMATION:  
 APPLICANT: Jewel Payne  
 APPLICANT: M. Keith Kennedy  
 APPLICANT: John Brooks Randall  
 APPLICANT: David Orlin Brower  
 APPLICANT: H. Ernest Schneff  
 TITLE OF INVENTION: *Bacillus thuringiensis* Isolates Active Against Cockroaches and Genes Encoding Cockroach-Act  
 TITLE OF INVENTION: Against Cockroaches and Genes Encoding Cockroach-Act  
 NUMBER OF SEQUENCES: 10  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: David R. Saliwanchik  
 STREET: 2421 N.W. 41st Street, Suite A-1  
 CITY: Gainesville  
 STATE: FL USA  
 COUNTRY: USA  
 ZIP: 32606  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/129, 610  
 FILING DATE:  
 CLASSIFICATION: 800  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/093, 199  
 FILING DATE: 15-JUL-1993  
 NAME:  
 PRIORITY DATA:  
 APPLICATION NUMBER: US 07/977, 350  
 FILING DATE: 17-NOV-1992  
 NAME:  
 PRIORITY DATA:  
 APPLICATION NUMBER: US 07/746, 751  
 FILING DATE: 21-AUG-1991  
 NAME:  
 PRIORITY DATA:  
 APPLICATION NUMBER: US 07/708, 266  
 FILING DATE: 28-MAY-1991  
 NAME:  
 PRIORITY DATA:  
 APPLICATION NUMBER: US 07/647, 399  
 FILING DATE: 29-JAN-1991  
 NAME:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Saliwanchik, David R.  
 REGISTRATION NUMBER: 31,794  
 REFERENCE/DOCKET NUMBER: MASS5CCD.C1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 904-75-8100  
 TELEFAX: 904-372-5800  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 222 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 HYPOTHETICAL: YES  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: *Bacillus thuringiensis*  
 SPRAIN: neoleoensis  
 INDIVIDUAL ISOLATE: PS20176  
 US-08-129-610-8

STATE: FL  
 COUNTRY: USA  
 ZIP: 32606  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/129,609A  
 FILING DATE: 30-SEP-1993  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/958,551  
 FILING DATE: 19-OCT-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/788,654  
 FILING DATE: 6-NOV-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Saliwanchik, David R.  
 REGISTRATION NUMBER: 31,794  
 REFERENCE/DOCKET NUMBER: M/J 101.02  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 904-375-8100  
 TELEFAX: 904-372-5800  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 222 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 HYPOTHETICAL: YES  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: *Bacillus thuringiensis*  
 STRAIN: neoleoensis  
 INDIVIDUAL ISOLATE: PS201T6  
 US-08-129-609A-8

Query Match 35.8%; Score 417; DB 1; Length 222;  
 Best Local Similarity 41.9%; Pred. No. 1.1e-34;  
 Matches 91; Conservative 42; Mismatches 72; Indels 12; Gaps 5;

Qy 15 DVVNYNSRIVQVA-PQYVNQALTLAKYFGQAI-----DGSTIRDFEKAHQIANDI-PQA 66  
 Db 6 DTTQLLITEITENPNTVLAQIAQAAAFQDALVPTETEFGEAIRFSMPKGLEVAKTIQPKG 65  
 Qy 67 AVNTLNQTVQGTQVSVMDKIVDINKNVLISIVDNKKEWDQTAAITNTFTNNSQ 126  
 Db 66 AAVAYTDTQLSQSNNNQVSMIDRVISLTKTVMGVALSG-SITQQTAAITDFTNNTQK 124  
 Qy 127 SBAWIFTYKEDAHKTSTYYNILFAQIDBETGGVMMATPLIAFDISVDEKEKVLFTYIKDT 186  
 Db 128 DSAWVFMGKETSHQTNTYNNMFAIQNETTERGVMMCPIGPEIRVFTDKRTVLFITQDY 184  
 Qy 187 ENYAVTYKAINVQVQALOSRSDSKVVD--AFKSPPHL 220  
 Db 185 ANYSVNTQTLRPAQPLIDSRLSINDLSEARSSKVL 221

RESULT 15  
 US-08-455-313-8  
 Sequence 8, Application US/08455313  
 Patent No. 5635480  
 GENERAL INFORMATION:  
 APPLICANT: Jewel Payne  
 APPLICANT: Kenneth Narva  
 APPLICANT: Kendrick Akira Uyeda  
 APPLICANT: Christine Julie Stalder  
 APPLICANT: Tracy Ellis Michaelis  
 TITLE OF INVENTION: No. 5635480el *Bacillus thuringiensis* Isolates and Toxins  
 NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: David R. Saliwanchik  
 STREET: 2421 N.W. 41st Street, Suite A-1  
 CITY: Gainesville  
 STATE: FL  
 ZIP: 32606  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/455,313  
 FILING DATE: 31-MAY-1995  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/129,610  
 FILING DATE: 30-SEP-1993  
 APPLICATION NUMBER: US 08/093,199  
 FILING DATE: 15-JUL-1993  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/977,350  
 FILING DATE: 17-NOV-1992  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/746,751  
 FILING DATE: 21-AUG-1991  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/708,266  
 FILING DATE: 28-MAY-1991  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/647,399  
 FILING DATE: 29-JAN-1991  
 CLASSIFICATION: 514  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Saliwanchik, David R.  
 REGISTRATION NUMBER: 31,794  
 REFERENCE/DOCKET NUMBER: MR55CCD.C1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 904-372-5800  
 TELEFAX: 904-372-5800  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 222 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: 222 amino acids  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 HYPOTHETICAL: YES  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: *Bacillus thuringiensis*  
 STRAIN: neoleoensis  
 INDIVIDUAL ISOLATE: PS201T6  
 US-08-455-313-8

Query Match 35.8%; Score 417; DB 1; Length 222;  
 Best Local Similarity 41.9%; Pred. No. 1.1e-34;  
 Matches 91; Conservative 42; Mismatches 72; Indels 12; Gaps 5;  
 15 DVVNYNSRIVQVA-PQYVNQALTLAKYFGQAI-----DGSTIRDFEKAHQIANDI-PQA 66  
 6 DTTQLLITEITENPNTVLAQIAQAAAFQDALVPTETEFGEAIRFSMPKGLEVAKTIQPKG 65  
 Qy 67 AVNTLNQTVQGTQVSVMDKIVDINKNVLISIVDNKKEWDQTAAITNTFTNNSQ 126  
 Db 66 AAVAYTDTQLSQSNNNQVSMIDRVISLTKTVMGVALSG-SITQQTAAITDFTNNTQK 124  
 Qy 127 SBAWIFTYKEDAHKTSTYYNILFAQIDBETGGVMMATPLIAFDISVDEKEKVLFTYIKDT 186  
 Db 128 DSAWVFMGKETSHQTNTYNNMFAIQNETTERGVMMCPIGPEIRVFTDKRTVLFITQDY 184  
 Qy 187 ENYAVTYKAINVQVQALOSRSDSKVVD--AFKSPPHL 220  
 Db 185 ANYSVNTQTLRPAQPLIDSRLSINDLSEARSSKVL 221

RESULT 15  
 US-08-455-313-8  
 Sequence 8, Application US/08455313  
 Patent No. 5635480  
 GENERAL INFORMATION:  
 APPLICANT: Jewel Payne  
 APPLICANT: Kenneth Narva  
 APPLICANT: Kendrick Akira Uyeda  
 APPLICANT: Christine Julie Stalder  
 APPLICANT: Tracy Ellis Michaelis  
 TITLE OF INVENTION: No. 5635480el *Bacillus thuringiensis* Isolates and Toxins  
 NUMBER OF SEQUENCES: 10

15 DVVNYNSRIVQVA-PQYVNQALTLAKYFGQAI-----DGSTIRDFEKAHQIANDI-PQA 66  
 6 DTTQLLITEITENPNTVLAQIAQAAAFQDALVPTETEFGEAIRFSMPKGLEVAKTIQPKG 65  
 67 AVNTLNQTVQGTQVSVMDKIVDINKNVLISIVDNKKEWDQTAAITNTFTNNSQ 126  
 66 AAVAYTDTQLSQSNNNQVSMIDRVISLTKTVMGVALSG-SITQQTAAITDFTNNTQK 124  
 Qy 127 SBAWIFTYKEDAHKTSTYYNILFAQIDBETGGVMMATPLIAFDISVDEKEKVLFTYIKDT 186

Qy 127 SBAWIFTYKEDAHKTSTYYNILFAQIDBETGGVMMATPLIAFDISVDEKEKVLFTYIKDT 186

Db 125 DSAWVPGKETSHQTNYYNNMFAIQNETTERGVMMCVPIGEIRVFTDKRTVLFLLTQDY 184  
Qy 187 ENYAVTVKAINVVAQALOSSRDSKVVD--AFKSPRHL 220  
Db 185 ANYSVNITQTLRFAQPLIDSRLSINDLSEALRSSKYI 221

Search completed: June 26, 2005, 16:07:05  
Job time : 45 secs



DT	15-JUL-1998 (Rel. 36, Created)	FT	TURN	238	Score 637; DB 1; Length 259;
DT	25-OCT-2004 (Rel. 45, Last sequence update)	SQ	SEQUENCE	259 AA:	29235 MW; 6924A01103D32B51 CRC64;
DB	Type-2Aa cytolytic delta-endotoxin (29 kDa cytolytic toxin).	Query Match	54.7%; Best Local Similarity 56.0%; Pred. No. 2; e=40;		
GN	Name=cyr2Aal; Synonyms=cytB;	Matches	126; Conservative 43; Mismatches 54; Indels 2; Gaps 2;		
OS	Bacillus thuringiensis (subsp. <i>kyushuensis</i> ).				
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.				
OX	NCBI_TaxID=44161;				
RN	[1]	QY	7 ITLTPSSDVNTSEIYQVAPQTYNQALTLAKYFQGAIDGSTLRFEXALQIANDIPOA 66		
RP	SEQUENCE FROM N.A. PubMed=8429550;	Db	31 IVLTPSSDLDNFNTVFPQQTINQALHLNAAQGADPLNLNFEXALQIANGIPMS 90		
RX	MedlineID=33156045; PubMed=8429550;	QY	67 AVNTLNQTVQQGTVQSYWMDKIVDMDKVNLSIVTDNKKPFDQVTAITNTFTNLNSQE 126		
RA	Koni P.A.; Ellar D.J.;	Db	91 AIVTLLNGSVIQTVETSYWVEQKQKTIQEVGLGVINSTSFWMNSVEATIKGTFNLDTQI 150		
RT	"Cloning and characterization of a novel <i>Bacillus thuringiensis</i> cytolytic delta-endotoxin."	QY	127 SEATFYYKEDAHKTYYNILPAQDEETGGMATAFLIAFDISVDEKPKRHKICSN 186		
RA	J. Mol. Biol. 229:319-327(1993).	Db	151 DEAMFWHSLSAINTSYYNILLSIQNETDGMAVPLAFAEVSDVVEQKVLFFTIRDS 210		
RN	[2]	QY	187 ENVTAVTKAINVYQALQSSRSKVYDAFK-SPRHLPRKRHKICSN 230		
RP	X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) MEDLINEID=96211639; PubMed=8632451; DOI=10.1006/jmbi.1996.0152;	Db	211 ARTEVOMKALTVQALHSS-NAPIVDIFNVNTNYLHSNHK1 QN 254		
RX	Li J., Koni P.A., Ellar D.J.;	QY			
RA	"Structure of the mosquitoicidal delta-endotoxin CytB from <i>Bacillus thuringiensis</i> sp. <i>kyushuensis</i> and implications for membrane pore formation."	Db			
RT	RT	QY			
RL	J. Mol. Biol. 257:129-152 (1996).	Db			
CC	-I- FUNCTION: Kills the larvae of dipteran insects by making pores in the epithelial cell membrane of the insect midgit.	RESULT 3			
CC	-I- SUBUNIT: Homodimer (protoxin) and monomer (active toxin).	Q71KW8	PRELIMINARY; ID Q71KW8; PRELIMINARY; PRT; 259 AA.		
CC	-I- DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of the spore coat.	AC	Q71KW8; AC		
CC	-I- PTM: Active after proteolytic processing.	DT	05-JUL-2004 (TREMBLrel. 27, Created)		
CC	-I- SIMILARITY: Belongs to the cycl/cy2 endotoxin family.	DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation - CC European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).	DB	05-JUL-2004 (TREMBLrel. 27, Last annotation update)		
CC	-----	OS	<i>Bacillus thuringiensis</i> (subsp. <i>darmstadiensis</i> ). Bacteria; Firmicutes; Bacillales; Bacillaceae; <i>Bacillus</i> .		
CC	-----	OC	SEQUENCE FROM N.A.		
CC	-----	OX	RC STRAIN=7-E10-2; PubMed=12520362;		
CC	-----	RN	RC PROMDONKOY B., CHAWAWIAT N., TANAPONGPIPAT S., LUXANANIL P., RA RA PANYI S.;		
CC	-----	RT	"Cloning and characterization of a cytolytic and mosquito larvical delta-endotoxin from <i>Bacillus thuringiensis</i> subsp. <i>darmstadiensis</i> ." RT CURR. MICROBIOL. 46:94-98 (2006).		
CC	-----	RL	DR EMBL: AF072606; AAC09631.1. -.		
CC	-----	DR	GO:0005576; C:extracellular; IEA.		
CC	-----	DR	GO:0009405; P:spore wall assembly (sensu Bacteria); IEA.		
CC	-----	DR	INTERPRO: IPR001615, Endotoxin_CytB.		
CC	-----	DR	PFAM: PF01338; Bac_thur_toxin_1.		
CC	-----	DR	PRODOM: PD00944; Endotoxin_CytB.		
CC	-----	SQ	SEQUENCE 259 AA: 29235 MW; 6924A01103D32B51 CRC64;		
DR	Z14147; CAA7519.1; -.	QY	7 ITLTPSSDVNTSEIYQVAPQTYNQALTLAKYFQGAIDGSTLRFEXALQIANDIPOA 66		
DR	S32432; S32432.	Db	31 IVLTPSSDLDNFNTVFPQQTINQALHLNAAQGADPLNLNFEXALQIANGIPMS 90		
DR	PIR: 1ICBY; X-ray; @=1-259.	QY	67 AVNTLNQTVQQGTVQSYWMDKIVDMDKVNLSIVTDNKKPFDQVTAITNTFTNLNSQE 126		
DR	PDB: 1ICBY; X-ray; @=1-259.	Db	91 AIVTLLNGSVIQTVETSYWVEQKQKTIQEVGLGVINSTSFWMNSVEATIKGTFNLDTQI 150		
DR	InterPro: IPR001615; Endotoxin_CytB.	QY	127 SEATFYYKEDAHKTYYNILPAQDEETGGMATAFLIAFDISVDEKPKRHKICSN 186		
DR	PFam: PF01338; Bac_thur_toxin_1.	Db	151 DEAMFWHSLSAINTSYYNILLSIQNETDGMAVPLAFAEVSDVVEQKVLFFTIRDS 210		
DR	ProDom; PD00944; Endotoxin_CytB; 1.	QY	187 ENVTAVTKAINVYQALQSSRSKVYDAFK-SPRHLPRKRHKICSN 230		
KW	3D-structure; Sporulation; Toxin.	Db	211 ARTEVOMKALTVQALHSS-NAPIVDIFNVNTNYLHSNHK1 QN 254		
FT	STRAND 44	FT	HELIX 51		
FT	STRAND 44	FT	HELIX 53		
FT	HELIX 54	FT	HELIX 63		
FT	STRAND 68	FT	HELIX 67		
FT	STRAND 70	FT	TURN 72		
FT	STRAND 75	FT	TURN 75		
FT	HELIX 77	FT	HELIX 84		
FT	TURN 85	FT	TURN 86		
FT	TURN 88	FT	TURN 89		
FT	STRAND 90	FT	TURN 106		
FT	HELIX 107	FT	TURN 122		
FT	HELIX 129	FT	TURN 141		
FT	TURN 142	FT	TURN 143		
FT	HELIX 146	FT	TURN 149		
FT	TURN 150	FT	TURN 151		
FT	TURN 153	FT	TURN 154		
FT	STRAND 155	FT	TURN 158		
FT	STRAND 165	FT	TURN 175		
FT	TURN 178	FT	TURN 182		
FT	STRAND 183	FT	TURN 183		
FT	HELIX 199	FT	HELIX 202		
FT	TURN 203	FT	TURN 204		
FT	STRAND 207	FT	TURN 208		
FT	STRAND 210	FT	TURN 225		
FT	HELIX 233	FT	HELIX 237		

RESULT 4		SEQUENCE FROM N.A.	
QBWNX0	PRELIMINARY;	PRT;	260 AA.
AC	QBNX0;		
DT	01-MAR-2002 (TREMBLrel. 20, Created)		
DT	01-MAR-2002 (TREMBLrel. 20, Last sequence update)		
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)		
DE	Cyt2Bc Protein.		
GN	Name=cyt2Bc;		
OS	Bacillus thuringiensis (subsp. medellin).		
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.		
OX	NCBI_TaxID=9672;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIGHT301;		
RA	Yu J.; Pang Y.;		
RT	"Cloning and expression of a cyt2Ba gene from Bacillus thuringiensis, strain T301."		
RT	Submitted (IDC-1999) to the EMBL/GenBank/DBJ databases.		
RL	-1- FUNCTION: Kills the larvae of dipteran insects by making pores in the epithelial cell membrane of the insect midgut (By similarity).		
CC	-1- DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of the spore coat.		
CC	-1- PM: Active after proteolytic processing (By similarity).		
CC	-1- SIMILARITY: Belongs to the cyt1/cyt2 endotoxin family.		
CC	--		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).		
CC	--		
DR	EMBL; US2043; AAB63254; 1; -.		
DR	EMBL; AF215645; AAP3722; 1; -.		
DR	HSSP; Q04470; ICBY.		
DR	InterPro; IPR001615; Endotoxin_CytB.		
DR	Pfam; PF01338; Bac_thur_toxin_1.		
DR	ProDom; PD009844; Endotoxin_CytB; 1.		
KW	Sporulation; Toxin.		
SEQUENCE	260 AA; 29843 MW; 47545F67B49EBAED CRC64;		
SQ	Query Match 51.1%; Score 595; DB 1; Length 263; Best Local Similarity 52.4%; Mismatches 44; Indels 62; Gaps 2; Matches 119; Conservative 52.4%; Pred. No. 4.4e-37;		
Qy	5 RVIITLTVPSSDVNVSEYQVAPQQYNGQALTAKYFOGAIDGSTLRDFEKALQIANDIP 64	5 RVIITLTVPSSDVNVSEYQVAPQQYNGQALTAKYFOGAIDGSTLRDFEKALQIANDIP 64	
Db	27 RHIALTVPSSTDITNFNEIYFVQYIAQALRLTNTFOGAIDPLTLNPNFEKALQIANGLP 86	30 RHIALTVPSSTDITNFNEIYFVQYIAQALRLTNTFOGAIDPLTLNPNFEKALQIANGLP 89	
Qy	65 QRAVNTLNQNTQQGTTVQSYSMIDKIVD1MKNVLS1VDNKKFWMDQTYTAATNTFTNLNS 124	65 QRAVNTLNQNTQQGTTVQSYSMIDKIVD1MKNVLS1VDNKKFWMDQTYTAATNTFTNLNS 124	
Db	87 NAGVTGTINQSOTHQTEISWMSIQKEITRSVGLVINSANFNNVSYSA1NTFTNLLEP 146	90 NAGVTGTINQSOTHQTEISWMSIQKEITRSVGLVINSANFNNVSYSA1NTFTNLLEP 149	
Qy	125 QSEBEAWTIVWRLSANCQTSSYYKLFQ1DEETGGVNMATLPIAFDISYDIEKEKVLPFTIK 184	125 QSEBEAWTIVWRLSANCQTSSYYKLFQ1DEETGGVNMATLPIAFDISYDIEKEKVLPFTIK 184	
Db	147 QVDENWIVWRLSANCQTSSYYKLFQ1DEETGGVNMATLPIAFDISYDIEKEKVLPFTIK 206	150 QVDENWIVWRLSANCQTSSYYKLFQ1DEETGGVNMATLPIAFDISYDIEKEKVLPFTIK 209	
Qy	185 DTENYAVTVAIKINVQVQALQSSRDSKVDYAFKSPPRH-LPRKRHKICSN 230	185 DTENYAVTVAIKINVQVQALQSSRDSKVDYAFKSPPRH-LPRKRHKICSN 230	
Db	207 DSARYEVTKMALKTvvQAl-DSTNAPIIDVENTHNSLHRPNTHILQN 252	210 DSARYEVTKMALKTvvQAl-DSTNAPIIDVENTHNSLHRPNHNLQN 255	

## RESULT 5

CYBA_BACTI		STANDARD		PRT;	263 AA.
ID	CYBA_BACTI				
AC	Q45723;				
DT	15-JUL-1998 (Rel. 36, Created)				
DT	15-JUL-1998 (Rel. 36, Last sequence update)				
DT	05-JUL-2004 (Rel. 44, Last annotation update)				
DB	Type-2Ba cytolytic delta-endotoxin (29 kDa cytolytic toxin).				
GN	Name=cyt2Bai; Synonyms=cyt2Ba, cytB;				
OS	Bacillus thuringiensis (subsp. israelensis).				
OC	Plasmid pR80.				
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.				
OX	NCBI_TaxID=1430;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIGHT4Q2;				
RX	Medline=97355937; PubMed=9212418;				
RA	Guerchicoff A., Ugalde R.A., Rubinstein C.P.;				
RT	"Identification and characterization of a cytolytic and mosquitoic delta-endotoxin from Bacillus thuringiensis subsp. jegathesan."				
RT	Appl. Environ. Microbiol. 63:3254-3260(1997).				
RL	Kills the larvae of dipteran insects by making pores in the epithelial cell membrane of the insect midgut (By similarity).				
CC	[2]				

## RESULT 6

CYBB_BACTJ		STANDARD		PRT;	263 AA.
ID	CYBB_BACTJ				
AC	Q32322;				
DT	30-MAY-2000 (Rel. 39, Created)				
DT	30-MAY-2004 (Rel. 39, Last sequence update)				
DT	05-JUL-2004 (Rel. 44, Last annotation update)				
DB	Type-2Bb cytolytic delta-endotoxin (30 kDa cytolytic toxin).				
GN	Name=cyt2Bbb.				
OS	Bacillus thuringiensis (subsp. jegathesan).				
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.				
OX	NCBI_TaxID=56955;				
RN	[1]				
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.				
RC	MBDLINE=97394931; PubMed=9251213;				
RA	Cheong H., Gill S.S.;				
RT	"Cloning and characterization of a cytolytic and mosquitoic delta-endotoxin from Bacillus thuringiensis subsp. jegathesan."				
RT	Appl. Environ. Microbiol. 63:3254-3260(1997).				
CC	[2]				

-!- DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of the spore coat.  
 CC -!- PTM: Active after proteolytic processing (By similarity).  
 CC -!- SIMILARITY: Belongs to the cyt/cyr2 endoxotoxin family.

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CC EMBL; U82519; AAB93477.1; -.  
 DR HSSP; Q04410; 1CBY.  
 DR InterPro; IPR001615; Endotoxin\_CytB.  
 DR Pfam; PF01338; Bac\_thur\_toxin\_1.  
 DR ProDom; P0009844; Endotoxin\_CytB; 1.  
 KW Direct protein sequencing; Sporulation; Toxin.

SEQUENCE 263 AA; 30059 MW; BDBB72CDB09D9D CRC64;  
 SQ Query Match Score 50.9%; DB 1; Length 263;  
 Best Local Similarity 55.2%; Pred. No. 6.7e-37;  
 Matches 116; Conservative 40; Mismatches 53; Indels 1; Gaps 1;

RESULT 8  
 CXAA\_BACTI ID CXAA\_BACTI STANDARD; PRT; 249 AA.  
 AC P05697; P05628;  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 13-AUG-1987 (Rel. 05, Last annotation update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DB Type-Iaa cytolytic delta-endotoxin (27 kDa cytolytic toxin).  
 GN Name-cytIaa; Synonyms=CytA;  
 OS Bacillus thuringiensis (subsp. *israelensis*), and  
 OS Bacillus thuringiensis (subsp. *morrisoni*).  
 OG Plasmid 72 Kb  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1430, 1441;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=B.t. *israelensis*;  
 MEDLINE=87086767; PubMed=3025452;  
 RX  
 RA Ward E.S., Ridley A.R., Ellar D.J.;  
 MEDLINE=87086764; PubMed=3025452;  
 RA Ward E.S., Ellar D.J.;  
 RT "Bacillus thuringiensis" var. *israelensis* delta-endotoxin. Nucleotide  
 sequence and characterization of the transcripts in *Bacillus*  
 thuringiensis and *Escherichia coli*.";  
 RL J. Mol. Biol. 191:1-11(1986).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=B.t. *israelensis*;  
 MEDLINE=87086767; PubMed=3025453;  
 RX  
 RA Ward E.S., Ridley A.R., Ellar D.J., Todd J.A.;  
 RT "Bacillus thuringiensis" var. *israelensis* delta-endotoxin. Cloning and  
 expression of the toxin in sporogenous and asporogenous strains of  
*Bacillus subtilis*."  
 RT J. Mol. Biol. 191:13-22(1986).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=B.t. *israelensis*, AND MUTAGENESIS.  
 RX  
 RA Ward E.S., Ridley A.R., Ellar D.J., Chilcott C.N.;  
 MEDLINE=89011377; PubMed=2845100;  
 RA Ward E.S., Ellar D.J., Chilcott C.N.;  
 RT "Single amino acid changes in the *Bacillus thuringiensis* var.  
*israelensis* delta-endotoxin affect the toxicity and expression of the  
 protein.";  
 RT J. Mol. Biol. 202:527-535(1988).  
 RL RN [4]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=B.t. *israelensis*;  
 MEDLINE=86016227; PubMed=4070003;  
 RX  
 RA Waaijik C.; Duilemans A.M., van Wolkum M.E.S., Visser B.;  
 DR "Molecular cloning and the nucleotide sequence of the Mr 28 000  
 crystal protein gene of *Bacillus thuringiensis* subsp. *israelensis*.";  
 RL Nucleic Acids Res. 13:8207-8217(1985).  
 RN [5]  
 RP REVISIONS TO 34-35;  
 RC SPECIES=B.t. *israelensis*;  
 RA Waaijik C.;  
 RL Submitted (FEB-1986) to the EMBL/GenBank/DDBJ databases.  
 RN [6]

Query Match Score 586; DB 2; Length 263;  
 Best Local Similarity 52.0%; Pred. No. 2.1e-36;  
 Matches 118; Conservative 44; Mismatches 63; Indels 2; Gaps 2;

RP	SEQUENCE FROM N.A. SPECIES=B.t.morroni; STRAIN=PG14; MEDLINE=87203386; PubMed=5575104;	DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)
RX		DB	Cytolytic toxin (Fragment)
RA		GN	Name=Cyt2Ba
PA	Bacillus thuringiensis var. morroni strain PG14: nucleotide sequence of a gene encoding a 27kDa crystal protein.;	OS	Bacillus thuringiensis (subsp. <i>tenebrionis</i> )
PA	"Bacillus thuringiensis" var. morroni strain PG14: nucleotide sequence of a gene encoding a 27kDa crystal protein.;	OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
RT	NCBP_TaxID=144;	OX	NCBI_TaxID=144;
PL		RN	
RP	SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.
RC	SPECIES=B.t.morroni; STRAIN=PG14;	RA	MEDLINE=97355937; PubMed=9212418;
CC	"Plasmid location, cloning, and sequence analysis of the gene encoding a 27.3-kilodalton cytoytic protein from <i>Bacillus thuringiensis</i> subsp. morrisoni (PG-14).";	RA	Guerlichoff A., Ugalde R.A., Rubinstein C.P.;
CC	Curr. Microbiol. 16:171-177(1987).	RT	"Identification and characterization of a previously undescribed cyt gene in <i>Bacillus thuringiensis</i> subsp. <i>israelensis</i> .";
RL	-1- PUNCTION: Kills the larvae of dipteran insects by making pores in the epithelial cell membrane of the insect midgut. Acts on mosquitoes and black flies.	RL	Appl. Environ. Microbiol. 63:2716-2721(1997).
CC	-1- DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of the spore coat.	EMBL	AF034926; AAC59344.1; -.
CC	-1- PTM: Active after proteolytic processing.	DR	HSSP: Q04470; 1CBY.
CC	-1- SIMILARITY: Belongs to the cyt/cyt2 endotoxin family.	GO	GO:0005516; C: extracellular; IEA.
CC		DR	GO: GO_0009405; Pathogenesis; IEA.
CC		DR	GO: GO_0042243; P: spore wall assembly (sensu Bacteria); IEA.
CC		DR	InterPro: IPR001615; Endotoxin_CytB.
CC		DR	Pfam: PF01338; Bac_thur_toxin; 1.
CC		DR	ProDom: PD009844; Endotoxin_CytB; 1.
CC		FT	NON-TER 1
CC		FT	NON-TER 157
CC		SQ	SEQUENCE 157 AA; 17716 MW; 7A00550DD3EB0124 CRC64;
CC			Query Match 38.5%; Score 448; DB 2; Length 157;
CC			Best Local Similarity 55.5%; Pred. No. 3e-26;
CC		Matches 86; Conservative 32; Mismatches 37; Indels 0; Gaps	Matches 86; Conservative 32; Mismatches 37; Indels 0; Gaps
CC		Qy	40 FQGAGDSTLRPDEKALQIANDPQAIVNTLNQTVQSYWMDKVIDMKVNL 99
CC		Db	3 FQGAGDPLTLNFNFKEALQIANGIPLNAGVTGTINQSVIQTIEVSVMISQKEIIRSVLG 62
CC		Qy	100 IVDINKRKEWDQTAITNTPTNNQSSEAWIIFYKEDAHRTSYNILLPAIQDBETGGV 15
CC		Db	63 IVDINSANTNSVSISSVATNTPTNLPQDVERWIVPNLSATQTSPYKILPSIQNDTGRF 12
CC		Qy	160 MATPIAFDISVDEKEKVLFWTTIKDTEYAVTK 194
CC		Db	123 MATPIAFITDVQKQQLFLITKDSARYEVNMK 157
CC			RESULT 10
CC		Q7BVD4	SEQUENCE FROM N.A.
CC		AC	MEDLINE=97355937; PubMed=9212418;
CC		DT	TREMBLrel. 27, Created)
CC		DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)
CC		DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)
CC		DE	"Identification and characterization of a previously undescribed cyt gene in <i>Bacillus thuringiensis</i> subsp. <i>israelensis</i> .";
CC		DR	Appl. Environ. Microbiol. 63:2716-2721(1997).
CC		EMBL	AF022886; AB76700.1; -.
CC		DR	GO: GO_0009405; Pathogenesis; IEA.
CC		DR	GO: GO_0042243; P: spore wall assembly (sensu Bacteria); IEA.
CC		DR	InterPro: IPR001615; Endotoxin_CytB.
CC		DR	Pfam: PF01338; Bac_thur_toxin; 1.
CC		DR	ProDom: PD009844; Endotoxin_CytB; 1.
CC		FT	NON-TER 1
CC		FT	NON-TER 157
CC		SQ	SEQUENCE 157 AA; 17716 MW; 7A00550DD3EB0124 CRC64;
CC			Query Match 38.5%; Score 448; DB 2; Length 157;
CC			Best Local Similarity 45.6%; Pred. No. 1.3e-26;
CC		Matches 99; Conservative 44; Mismatches 64; Indels 10; Gaps 5;	Matches 99; Conservative 44; Mismatches 64; Indels 10; Gaps 5;
CC		Qy	5 RVITLTVP-S-DVVNVYSEIYGV-APOVYNQNALTAKYFGQAI-----DGSTLRFDFEKA 56
CC		DB	116 TNTFTNLSNSEAWIIFYKEDAHKTSYNILLFAIQDETGVWMTLPIAFDISYDIKE 175
CC		Qy	144 INTFTNLSNSEAWIIFYKEDAHKTSYNILLFAIQDETGVWMTLPIAFDISYDIKE 175
CC		DB	144 INTFTNLSNSEAWIIFYKEDAHKTSYNILLFAIQDETGVWMTLPIAFDISYDIKE 175
CC		Qy	176 EKVLFVTTIKDTEYAVTKAINVYQALQSSRSKIVTD 212
CC		DB	204 EQVLFITQDASVNVNIQSLKFAQPLVSSSQYPA 240
CC			RESULT 9
CC		ID	052298
CC		PRELIMINARY;	PRELIMINARY;
CC		PRT;	157 AA.
CC			052298; 01-JUN-1998 (TREMBLrel. 06, Created)
CC			052298; 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
CC		DT	052298; 01-JUN-1998 (TREMBLrel. 06, Last sequence update)

Best Local Similarity 55.5%; Pred. No. 3e-26;	Matches 86; Conservative 32; Mismatches 37; Indels 0; Gaps 0;	Bacillus thuringiensis.
Matches 86; Conservative 32; Mismatches 37; Indels 0; Gaps 0;	OC Bacteria: Firmicutes; Bacillales; Bacillaceae; Bacillus. NCBI_TaxID=1428;	OS OC Bacteria: Firmicutes; Bacillales; Bacillaceae; Bacillus. NCBI_TaxID=1428; RN [1]
Qy 40 FGAGDGSTRFDFEKALQIANDIPOAAVNTLNQTVQSVMDKIVDIMKNTLS 99	RQ STRAIN=4KL;	RP SEQUENCE FROM N.A.
Db 3 FGAGDPLTINFNFEKALQIANGLNPAGTGTINGSVMIKETRSVLG 62	RX MEDLINE=97355937; PubMed=9212418;	RA Guerchicoff A., Ugale R.A., Rubinstein C.P.;
Qy 100 IVIDNKKFWDOYTAATNTPTNLNSOEAWIIFYKEDAHKTYYNNILFAIQDEBTGGV 159	RT "Identification and characterization of a previously undescribed cyt gene in <i>Bacillus thuringiensis</i> subsp. <i>israelensis</i> .";	RT
Db 63 LVNSANFNVSVSALTNTPTNLNEPDENWVNRLSATQTSIFYKILFSIQNEDTGRF 122	Appl. Environ. Microbiol. 63:2716-2721(1997).	RT
Qy 160 MATLPIAFDISVDEKEKLFVTIKDTENYAVK 194	DR EMBL: AF022884; AAB87598.1; -.	DR
Db 123 MAILPIAEIFTVDQKQQLFPTIKDSARVEVKM 157	DR HSSP; Q04470; 1CBY.	DR
RESULT 11	DR GO; GO:0005576; C:extracellular; IEA.	DR GO; GO:0009405; P:pathogenesis; IEA.
ID O30895 PRELIMINARY; PRT; 156 AA.	DR GO; GO:0042243; P:spore wall assembly (sensu Bacteria); IEA.	DR InterPro: IPR001615; Endotoxin_CytB.
AC O30895_1 PRELIMINARY; PRT; 156 AA.	DR Pfam: PF01338; Bac_thur_toxin_1.	DR ProDom: PD00944; Endotoxin_CytB; 1.
DT 01-JAN-1998 (TREMBLrel. 05, Created)	FT NON TER 1	FT NON TER 1
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)	FT SEQ 156 AA; 156 AA; 156 MW; 80550DD3E8A12413 CRC64;	FT SEQ 156 AA; 156 MW; 80550DD3E8A12413 CRC64;
DE Cytolytic toxin homolog (Fragment).	Query Match 38.0%; Score 443; DB 2; Length 156;	Query Match 38.0%; Score 443; DB 2; Length 156;
OS Bacillus thuringiensis (subsp. <i>israelensis</i> ).	Best Local Similarity 55.9%; Pred. No. 7.2e-26;	Best Local Similarity 55.9%; Pred. No. 7.2e-26;
OC Bacteria: Firmicutes; Bacillales; Bacillaceae; Bacillus.	Mismatches 31; Mismatches 36; Indels 0; Gaps 0;	Mismatches 31; Mismatches 36; Indels 0; Gaps 0;
NCBI_TaxID=1430;	FT NON TER 1	FT NON TER 1
RN [1]	FT SEQ 156 AA; 156 MW; 80550DD3E8A12413 CRC64;	FT SEQ 156 AA; 156 MW; 80550DD3E8A12413 CRC64;
RP SEQUENCE FROM N.A.	Query Match 38.0%; Score 443; DB 2; Length 156;	Query Match 38.0%; Score 443; DB 2; Length 156;
RC STRAIN=PG14;	DB 3 PQGAIQPLTINFNFEKALQIANGLNPAGTGTINGSVMIKETRSVLG 62	DB 3 PQGAIQPLTINFNFEKALQIANGLNPAGTGTINGSVMIKETRSVLG 62
RX MEDLINE=97355937; PubMed=9212418;	Qy 100 IVIDNKKFWDOYTAATNTPTNLNSQEAWIIFYKEDAHKTYYNNILFAIQDEBTGGV 159	Qy 100 IVIDNKKFWDOYTAATNTPTNLNSQEAWIIFYKEDAHKTYYNNILFAIQDEBTGGV 159
RA Guerchicoff A., Ugale R.A., Rubinstein C.P.;	DR 63 LVNSANFNVSVSALTNTPTNLNEPDENWVNRLSATQTSIFYKILFSIQNEDTGRF 122	DR 63 LVNSANFNVSVSALTNTPTNLNEPDENWVNRLSATQTSIFYKILFSIQNEDTGRF 122
RT "Identification and characterization of a previously undescribed cyt gene in <i>Bacillus thuringiensis</i> subsp. <i>israelensis</i> .";	Qy 160 MATLPIAFDISVDEKEKLFVTIKDTENYAV 191	Qy 160 MATLPIAFDISVDEKEKLFVTIKDTENYAV 191
DE Cytolytic toxin homolog (Fragment).	DR 123 MAILPIAEIFTVDQKQQLFPTIKDSARVEV 154	DR 123 MAILPIAEIFTVDQKQQLFPTIKDSARVEV 154
OS Bacillus thuringiensis.	RESULT 13	RESULT 13
NCBI_TaxID=1430;	ID O30969 PRELIMINARY; PRT; 156 AA.	ID O30969 PRELIMINARY; PRT; 156 AA.
RN [1]	AC O30969; DT 01-JAN-1998 (TREMBLrel. 05, Created)	AC O30969; DT 01-JAN-1998 (TREMBLrel. 05, Created)
RP SEQUENCE FROM N.A.	DR Pfam: PF01338; Bac_thur_toxin_1.	DR Pfam: PF01338; Bac_thur_toxin_1.
RX MEDLINE=97355937; PubMed=9212418;	DR ProDom: PD00944; Endotoxin_CytB; 1.	DR ProDom: PD00944; Endotoxin_CytB; 1.
RA Guerchicoff A., Ugale R.A., Rubinstein C.P.;	FT NON TER 1	FT NON TER 1
RT "Identification and characterization of a previously undescribed cyt gene in <i>Bacillus thuringiensis</i> subsp. <i>israelensis</i> .";	FT SEQ 156 AA; 156 MW; 80478F13E8A13B0C CRC64;	FT SEQ 156 AA; 156 MW; 80478F13E8A13B0C CRC64;
DE Putative cytolytic toxin (Fragment).	DB 3 PQGAIQPLTINFNFEKALQIANGLNPAGTGTINGSVMIKETRSVLG 62	DB 3 PQGAIQPLTINFNFEKALQIANGLNPAGTGTINGSVMIKETRSVLG 62
GN Name=cyt2Ba;	Qy 100 IVIDNKKFWDOYTAATNTPTNLNSQEAWIIFYKEDAHKTYYNNILFAIQDEBTGGV 159	Qy 100 IVIDNKKFWDOYTAATNTPTNLNSQEAWIIFYKEDAHKTYYNNILFAIQDEBTGGV 159
OC Bacteria: Firmicutes; Bacillales; Bacillaceae; Bacillus.	DR 63 LVNSANFNVSVSALTNTPTNLNEPDENWVNRLSATQTSIFYKILFSIQNEDTGRF 122	DR 63 LVNSANFNVSVSALTNTPTNLNEPDENWVNRLSATQTSIFYKILFSIQNEDTGRF 122
NCBI_TaxID=1428;	Qy 160 MATLPIAFDISVDEKEKLFVTIKDTENYAV 191	Qy 160 MATLPIAFDISVDEKEKLFVTIKDTENYAV 191
RN [1]	DR 123 MAILPIAEIFTVDQKQQLFPTIKDSARVEV 154	DR 123 MAILPIAEIFTVDQKQQLFPTIKDSARVEV 154
RP SEQUENCE FROM N.A.	RESULT 12	RESULT 12
RX MEDLINE=97355937; PubMed=9212418;	ID Q9R9CO PRELIMINARY; PRT; 156 AA.	ID Q9R9CO PRELIMINARY; PRT; 156 AA.
RA Guerchicoff A., Ugale R.A., Rubinstein C.P.;	DR 01-MAY-2000 (TREMBLrel. 13, Created)	DR 01-MAY-2000 (TREMBLrel. 13, Created)
RT "Identification and characterization of a previously undescribed cyt gene in <i>Bacillus thuringiensis</i> subsp. <i>israelensis</i> .";	DR 01-OCT-2003 (TREMBLrel. 25, Last annotation update)	DR 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Putative cytolytic toxin (Fragment).	DR HSSP; Q04470; 1CBY.	DR HSSP; Q04470; 1CBY.
GN Name=cyt2Ba;	DR GO; GO:0005576; C:extracellular; IEA.	DR GO; GO:0009405; P:pathogenesis; IEA.
NCBI_TaxID=1428;	DR InterPro: IPR001615; Endotoxin_CytB.	DR InterPro: IPR001615; Endotoxin_CytB.
RN [1]	DR Pfam: PF01338; Bac_thur_toxin_1.	DR Pfam: PF01338; Bac_thur_toxin_1.
RP SEQUENCE FROM N.A.	DR ProDom: PD00944; Endotoxin_CytB; 1.	DR ProDom: PD00944; Endotoxin_CytB; 1.
RX MEDLINE=97355937; PubMed=9212418;	FT NON TER 1	FT NON TER 1
RA Guerchicoff A., Ugale R.A., Rubinstein C.P.;	FT SEQ 156 AA; 17574 MW; 80478F13E8A13B0C CRC64;	FT SEQ 156 AA; 17574 MW; 80478F13E8A13B0C CRC64;
RT "Identification and characterization of a previously undescribed cyt gene in <i>Bacillus thuringiensis</i> subsp. <i>israelensis</i> .";	DB 3 PQGAIQPLTINFNFEKALQIANGLNPAGTGTINGSVMIKETRSVLG 62	DB 3 PQGAIQPLTINFNFEKALQIANGLNPAGTGTINGSVMIKETRSVLG 62
DE Putative cytolytic toxin (Fragment).	Qy 100 IVIDNKKFWDOYTAATNTPTNLNSQEAWIIFYKEDAHKTYYNNILFAIQDEBTGGV 159	Qy 100 IVIDNKKFWDOYTAATNTPTNLNSQEAWIIFYKEDAHKTYYNNILFAIQDEBTGGV 159
GN Name=cyt2Ba;	DR 63 LVNSANFNVSVSALTNTPTNLNEPDENWVNRLSATQTSIFYKILFSIQNEDTGRF 122	DR 63 LVNSANFNVSVSALTNTPTNLNEPDENWVNRLSATQTSIFYKILFSIQNEDTGRF 122
OC Bacteria: Firmicutes; Bacillales; Bacillaceae; Bacillus.	Qy 160 MATLPIAFDISVDEKEKLFVTIKDTENYAV 191	Qy 160 MATLPIAFDISVDEKEKLFVTIKDTENYAV 191
NCBI_TaxID=1428;	DR 123 MAILPIAEIFTVDQKQQLFPTIKDSARVEV 154	DR 123 MAILPIAEIFTVDQKQQLFPTIKDSARVEV 154

Matches 84; Conservative 32; Mismatches 36; Indels 0; Gaps 0;

Qy 40 FGGAGIDGSTLRRPDEKALQIANDIPOQA VVNTLNQTVQGTVQSYMDKIVDIMKNTS 99  
Db 3 FGGAGIDPLTLNPFNEKALQIANGIPNQAGTGTINOSVTHOTIEVSVMISQKEIIIRSLTG 62

Qy 100 IVDNKKFWDQVTAITFTNNISQS EAWIIFYKEDAHKTSTYYNLLPAIODEETCGV 159  
Db 63 LVINSANFTNSVMSAINTPTNLEPQVDTENWVWRNLSATQTSYKILFSONEDTGRF 122

Qy 160 MATLPIAFADISVDPTEKEVLFVTTIKDTENYAV 191  
Db 123 MATLPIAFBITEVDVQKQQLLFITKDSARYEV 154

**RESULT 14**  
CBAB\_BACTW ID\_CBAB\_BACTW STANDARD; PRT; 265 AA.  
AC Q45790; DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DR DE Type-1Ba cytolytic delta-endotoxin.  
GN Name=cyc1Ba;  
OS Bacillus thuringiensis (subsp. neoleensis).  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TAXID=43262;  
RN [1] RP SEQUENCE FROM N.A.

CC -I- SEQUENCE FROM N.A.  
RC STRAIN=PS20116;  
RA Narva K.E.; Payne J.M.; Uyeda K.A.; Stalder C.J.; Michaels T.B.;  
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.  
CC -I- FUNCTION: Kills the larvae of dipteran insects by making pores in the epithelial cell membrane of the insect mid gut (By similarity).  
CC -I- DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of the spore coat.  
CC -I- SIMILARITY: Belongs to the cyt1/cyt2 endotoxin family.  
CC -I- PRT: Active after proteolytic processing.  
CC -I- SIMILARITY: Belongs to the cyt1/cyt2 endotoxin family.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions. There are no restrictions on its modification and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.ibb-sib.ch/announce/> or send an email to license@ibb-sib.ch).

CC DR EMBL; U37196; AA03693.1; -.  
HSSP: Q04470; ICBY.  
InterPro: IPR001615; Endotoxin\_CytB.  
DR Ptam; P01338; Bac\_thur\_toxin\_CytB.  
DR ProDom; PDD09844; Endotoxin\_CytB; 1.  
KW Sporulation; Toxin.  
SEQUENCE 265 AA; 29906 MW; 260D1495F8C477A2 CRC64;

Query Match 36.4%; Score 423.5; DB 1; Length 265;  
Best Local Similarity 40.9%; Pred. No. 4.1e-2;  
Matches 94; Conservative 47; Mismatches 72; Indels 17; Gaps 6;

Qy 5 RYITLTVPSSDVNV-NQAVVNTLNQTVQGTVQSYMDKIVDIMKNTSIVIDNKKFWQVT 54  
Db 38 RYIYKV--KDPIDTDTQLEITIEENPVYQLOIQLAAQDQDLVPTETRCEAIRFMP 95

Qy 55 KALQIANDI-PQAAVNTLNQTVQGTVQSYMDKIVDIMKNTSIVIDNKKFWQVT 113  
Db 96 KGLEVAKTIQPKGAVVAYTDQTLQSNNQVSYMDRVTSVLKTMGVLSG-SITQFTA 154

Qy 114 ATINTTPFLNSQSEAWIIFYKEDAHKTSTYYNLLPAIODEETCGVMTLPADFSYDI 173  
Db 155 AITDTFTNLNTQKDSAWVFGETSHTQNTNTVNMFQIQNFTGRYMMCFPGEIRVFT 214

Qy 174 EKEKVLFVTTIKDTENYAVTKAINVQALQSSRSKIVVD--AFKSPRHL 220

Db 215 DKRTPLUTTDYANYSVNIQTRFAQPLIDSRLALSINDLSEARSSSKYL 264

**RESULT 15**  
CBAB\_BACTV ID\_CBAB\_BACTV STANDARD; PRT; 250 AA.  
AC P94594; DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DR DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DB Type-1ab cytolytic delta-endotoxin (27 kDa cytolytic toxin).  
GN Name=cyt1Ab1;  
OS Bacillus thuringiensis (subsp. medellin).  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TAXID=79672;  
RN [1] RP SEQUENCE FROM N.A.  
RC STRAIN=H30 / 163-131;  
RX MEDLINE=97176379; PubMed=9023925;  
RA Thiery I.; Delecluse A.; Tamayo M.C.; Ordzu S.;  
RT "Identification of a gene for Cytia-like hemolysin from *Bacillus thuringiensis* subsp. medellin and expression in a crystal-negative B. thuringiensis strain.";  
RT Appl. Environ. Microbiol. 63:468-473 (1997).  
RL CC -I- FUNCTION: Kills the larvae of dipteran insects by making pores in the epithelial cell membrane of the insect mid gut.  
CC -I- DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of the spore coat.  
CC -I- PRT: Active after proteolytic processing.  
CC -I- SIMILARITY: Belongs to the cyt1/cyt2 endotoxin family.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions. There are no restrictions on its modification and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.ibb-sib.ch/announce/> or send an email to license@ibb-sib.ch).

CC DR EMBL; X98793; CRA67328.1; -.  
DR HSSP: Q04470; ICBY.  
DR InterPro: IPR001615; Endotoxin\_CytB.  
DR Pfam; PF01338; Bac\_thur\_toxin\_1.  
DR ProDom; PDD09844; Endotoxin\_CytB; 1.  
KW Sporulation; Torin. 27507 MW; A57164B0B2C7AEF6 CRC64;  
SEQUENCE 250 AA;

Query Match 35.8%; Score 416.5; DB 1; Length 250;  
Best Local Similarity 41.4%; Pred. No. 1.3e-23;  
Matches 91; Conservative 52; Mismatches 62; Indels 15; Gaps 6;

Qy 5 RYITLTVPSSDVNV---YSEIYQAVQPYQVNOQALTLAKYFOCA-IDGST---LRDFP 53  
Db 25 RVITLRIDDPNEINNLNSINET--NYLQOAIMLANAFQKALVPTSTEFAEDALQFSM 82

Qy 54 EKALQIANDI-PQAAVNTLNQTVQGTVQSYMDKIVDIMKNTSIVIDNKKFWQVT 112  
Db 83 TKGLEVANTISPQGAVVAYTDQTLQSNNQVSYMDRVTSVLKTMGVLSG-QSVIEQLT 141

Qy 113 AAITNTTPFLNSQSEAWIIFYKEDAHKTSTYYNLLPAIODEETCGVMTLPADFSYDI 172  
Db 142 SAVNTTFTNLNTQKDSAWVFGETSHTQNTNTVNMFQIQNFTGRYMMCFPGEIRVFT 201

Qy 173 EKEKVLFVTTIKDTENYAVTKAINVQALQSSRSKIVVD 212  
Db 202 AVKERVFLFTQDSASVNTVNQTSLIKFAQPLVSASEVPIAD 241

Search completed: June 26, 2005, 16:05:31  
Job time : 177 sec

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M Protein - protein search, using SW model									
GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.									
run on: June 26, 2005, 15:59:48 ; Search time 159 Seconds (without alignments) 558.683 Million cell updates/sec									
title: US-10-767-605-2									
effect score: 1165 sequence: 1 MFFNRVITLTVPSDVNYS.....DAFKSPRHLPRKRHKICNS 231									
scoring table: BLOSUM62 Gapext 10.0 , Gapext 0.5									
searched: 1717557 seqs, 384547976 residues									
total number of hits satisfying chosen parameters: 1717557									
minimum DB seq length: 0 maximum DB seq length: 2000000000									
post-processing: Minimum Match 0% Maximum Match 100% Listing First 45 summaries									
database : Published Applications_AAA: 1: /cgn2_6/ptodata/2/pubpaas/us07_pubcomb.pep; 2: /cgn2_6/ptodata/2/pubpaas/pct_new_pub.pep; 3: /cgn2_6/ptodata/2/pubpaas/us06_new_pub.pep; 4: /cgn2_6/ptodata/2/pubpaas/us06_pubcomb.pep; 5: /cgn2_6/ptodata/2/pubpaas/us07_new_pub.pep; 6: /cgn2_6/ptodata/2/pubpaas/pctus_pubcomb.pep; 7: /cgn2_6/ptodata/2/pubpaas/us08_new_pub.pep; 8: /cgn2_6/ptodata/2/pubpaas/us09_pubcomb.pep; 9: /cgn2_6/ptodata/2/pubpaas/us09b_pubcomb.pep; 10: /cgn2_6/ptodata/2/pubpaas/us09c_pubcomb.pep; 11: /cgn2_6/ptodata/2/pubpaas/us10_new_pub.pep; 12: /cgn2_6/ptodata/2/pubpaas/us10a_pubcomb.pep; 13: /cgn2_6/ptodata/2/pubpaas/us10b_pubcomb.pep; 14: /cgn2_6/ptodata/2/pubpaas/us10c_pubcomb.pep; 15: /cgn2_6/ptodata/2/pubpaas/us10d_pubcomb.pep; 16: /cgn2_6/ptodata/2/pubpaas/us11_new_pub.pep; 17: /cgn2_6/ptodata/2/pubpaas/us11b_pubcomb.pep; 18: /cgn2_6/ptodata/2/pubpaas/us11c_new_pub.pep; 19: /cgn2_6/ptodata/2/pubpaas/us11a_pubcomb.pep; 20: /cgn2_6/ptodata/2/pubpaas/us11_new_pub.pep; 21: /cgn2_6/ptodata/2/pubpaas/us60_new_pubcomb.pep; 22: /cgn2_6/ptodata/2/pubpaas/us60_pubcomb.pep;									
RESULT 1 US-10-316-972-2 ; Sequence 2, Application US/10316972 ; Publication No. US20030167521A1 ; GENERAL INFORMATION: ; APPLICANT: Rupar, Mark J. ; APPLICANT: Donovan, William P. ; APPLICANT: Tan, Yuping ; APPLICANT: Slaney, Annerte C. ; TITLE OF INVENTION: Bacillus thuringiensis CryET29 Compositions Toxic to Coleoptera and Osteocophalides spp. ; TITLE OF INVENTION: Insects and Osteocophalides spp. ; FILE REFERENCE: MECO-071-2 ; CURRENT APPLICATION NUMBER: US/10/386,972 ; CURRENT FILING DATE: 2003-03-12 ; PRIOR APPLICATION NUMBER: 09/611,216 ; PRIOR FILING DATE: 2000-07-06 ; PRIOR APPLICATION NUMBER: 08/721,259 ; PRIOR FILING DATE: 1996-09-26 ; NUMBER OF SEQ ID NOS: 4 ; SOFTWARE: PatentIn version 3.2 ; SEQ ID NO 2 ; LENGTH: 231 ; TYPE: PRT ; ORGANISM: Bacillus thuringiensis									
SUMMARIES									
Pred. No. 18 the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution.									
result No. Score Match Length DB ID Description									
1	1165	100.0	231	14	US-10-386-972-2	Sequence 2, Appli	Score 1165; DB 14; Length 231;		
2	1165	100.0	231	16	US-10-767-605-2	Sequence 2, Appli	Pred. No. 2. e-99;		
3	101	8.7	477	15	US-10-335-977-9400	Sequence 9, Appli	Mismatches 0; Indels 0; Gaps 0		
4	97	8.3	1833	8	US-08-945-567D-4	Sequence 4, Appli			
5	97	8.3	1833	14	US-10-175-282-4	Sequence 4, Appli			
6	97	8.3	1833	14	US-10-175-275-4	Sequence 3, Appli			
7	97	8.3	1992	8	US-08-945-567D-3	Sequence 3, Appli			
8	97	8.3	1992	8	US-08-621-944A-3	Sequence 3, Appli			
9	97	8.3	1992	14	US-10-175-275-3	Sequence 3, Appli			
10	97	8.3	1992	14	US-10-175-275-3	Sequence 3, Appli			
11	97	8.3	1992	14	US-10-175-275-3	Sequence 3, Appli			

RESULT 2  
 US 10-767-605-2  
 / Sequence 2, Application US/10767605  
 / Publication No. US20040127695A1.  
 / GENERAL INFORMATION:  
 / APPLICANT: Rupar, Mark J.  
 / APPLICANT: Donovan, William P.  
 / APPLICANT: Tan, Yiping  
 / APPLICANT: Sianey, Annette C.  
 / TITLE OF INVENTION: Plants Toxic to Coleopteran Insects and Ctenocephalides spp.  
 / FILE REFERENCE: MECO:017--3  
 / CURRENT APPLICATION NUMBER: US/10/767,605  
 / CURRENT FILING DATE: 2004-01-29  
 / PRIOR APPLICATION NUMBER: 10/386,972  
 / PRIOR FILING DATE: 2003-03-12  
 / PRIOR APPLICATION NUMBER: 09/611,216  
 / PRIOR FILING DATE: 2000-07-06  
 / PRIOR APPLICATION NUMBER: 08/721,259  
 / PRIOR FILING DATE: 1996-09-26  
 / NUMBER OF SEQ ID NOS: 4  
 / SOFTWARE: PatentIn version 3.2  
 / SEQ ID NO: 2  
 / LENGTH: 231  
 / TYPE: PRT  
 / ORGANISM: *Bacillus thuringiensis*  
 / US-10-767-605-2

Query Match 100.0% Score 1165; Length 231;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-99;  
 Matches 231; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 MFENRVLITLVESSDVNNYSEIYQAVQYNNQALTLAKYFQGAIDSTLRDPFKQLQIA 60  
 Db 1 MFENRVLITLVESSDVNNYSEIYQAVQYNNQALTLAKYFQGAIDSTLRDPFKQLQIA 60

Qy 61 NDIPQAAVNTLNQTYQOGTIVQSYWMIDKIVDIMKVNLSIVIDNKKFWQVTAATNTFT 120  
 Db 61 NDIPQAAVNTLNQTYQOGTIVQSYWMIDKIVDIMKVNLSIVIDNKKFWQVTAATNTFT 120

Qy 121 NUNSQESEAWIIFYKEDAHKTTSYYNNLFQIAQDEETGGVMMATLPFTAIDSYDIEKEKVLF 180  
 Db 121 NUNSQESEAWIIFYKEDAHKTTSYYNNLFQIAQDEETGGVMMATLPFTAIDSYDIEKEKVLF 180

Qy 181 VTIKDNEYAVTVKAINVQALLOSSRSKVDAFKSPRHLPRKRHKICNS 231  
 Db 181 VTIKDNEYAVTVKAINVQALLOSSRSKVDAFKSPRHLPRKRHKICNS 231

RESULT 3  
 US 10-335-977-9400  
 / Sequence 9400, Application US/10335977  
 / Publication No. US20040052795A1.  
 / GENERAL INFORMATION:  
 / APPLICANT: DOUGLAS SMITH et al  
 / TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES  
 / RELATING TO HELICOBACTER PYLORI FOR  
 / DIAGNOSTICS AND THERAPEUTICS  
 / NUMBER OF SEQUENCES: 10031  
 / CORRESPONDENCE ADDRESS:

RESULT 4  
 US 08-945-567D-4  
 / Sequence 4, Application US/08945567D  
 / Publication No. US20010014672A1.  
 / GENERAL INFORMATION:  
 / APPLICANT: SASAKI, Ken  
 / APPLICANT: HARKNESS, Robin E.  
 / APPLICANT: LOOSHORE, Sheena M.  
 / APPLICANT: CHONG, Pele  
 / APPLICANT: KLEIN, Michel H.  
 / TITLE OF INVENTION: HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE PROTEIN OF  
 / MORAXELLA  
 / FILE REFERENCE: 1038-745 MIS



RESULT 7  
 US-10-175-275-4  
 ; Sequence 4, Application US/10175275  
 ; Publication No. US200301712541  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SASAKI, Ken  
 ; APPLICANT: HARNES, Robin E.  
 ; APPLICANT: LOOSMORE, Sheena M.  
 ; APPLICANT: CHONG, Pele  
 ; APPLICANT: KLEIN, Michel H.  
 ; TITLE OF INVENTION: HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE PROTEIN OF  
 ; FILE REFERENCE: 1038-745 MIS  
 ; CURRENT APPLICATION NUMBER: US/08/945, 567D  
 ; CURRENT FILING DATE: 1996-04-29  
 ; PRIOR APPLICATION NUMBER: 08/431,718  
 ; PRIOR FILING DATE: 1995-05-01  
 ; PRIOR APPLICATION NUMBER: 08/478,370  
 ; PRIOR FILING DATE: 1995-06-07  
 ; PRIOR APPLICATION NUMBER: 08/621,944  
 ; PRIOR FILING DATE: 1996-03-26  
 ; PRIOR APPLICATION NUMBER: PCT/CA96/00264  
 ; NUMBER OF SEQ ID NOS: 10  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 3  
 ; LENGTH: 1992  
 ; TYPE: PRT  
 ; ORGANISM: Moraxella catarrhalis  
 ; US-08-945-567D-3

Query Match 8.3%; Score 97; DB 8; Length 1992;  
 Best Local Similarity 22.8%; Pred. No. 23;  
 Matches 50; Conservative 40; Mismatches 93; Indels 36; Gaps 7;  
 ;

Qy 13 SSDVNVYSEIYQVAPQYVNONALTLARYFOGAIDGSTLRFDEKALQIAN----- 61  
 Db 1057 SHDAVTGGKIVDLKLTKLENKISSTATKAQNLHBSVADEQGNNTTVSNPSSYDTSKTS 1116  
 Qy 62 DIPQAAVNTLNQTYQGTVQSYMIDKLYDIMK-----NVLSVIDDNKKFWDQVTAII 115  
 Db 1117 DVTPAGENGTTKNGKVVRVGQTKGLTTPKLTVGNNNGKG-VIDSONGQNTIT-GL 1175  
 Qy 116 TNTFTNLNSQESEAWIIFYKEDAHHTSYNNILFQDDE--TGGVMTAPIADFDISVD 172  
 Db 1176 SNTLLANVTDKGSV-----RTTEQNI--IKDEDKTRASIVDVLSAGPNLQGN 12224  
 Qy 173 IEKEVYLFLPTIKDTENYATVKAIVNVAQLSRSRQKV 211  
 Db 1223 -GEAVDFVSTYDTVNFDGNATTAKVYDDTSKTV 1259

RESULT 9  
 US-08-621-944A-3  
 ; Sequence 3, Application US/08621944A  
 ; Publication No. US2002068070A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SASAKI, Ken  
 ; APPLICANT: HARNES, Robin E.  
 ; APPLICANT: LOOSMORE, Sheena M.  
 ; APPLICANT: CHONG, Pele  
 ; TITLE OF INVENTION: HIGH MOLECULAR WEIGHT MAJOR OUTER  
 ; NUMBER OF SEQUENCES: 10  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Sim & McBurney  
 ; STREET: Suite 701, 330 University Avenue  
 ; CITY: Toronto  
 ; STATE: Ontario  
 ; COUNTRY: Canada  
 ; ZIP: M5G 1R7  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC Compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:

RESULT 8  
 US-08-945-567D-3  
 ; Sequence 3, Application US/08945567D  
 ; Publication No. US2001014672A1

APPLICATION NUMBER: US/08/621,944A  
 FILING DATE: 26-MAR-1996  
 CLASSIFICATION:  
   APPLICATION NUMBER: US 08/478,370  
   FILING DATE: 07-JUN-1995  
 CLASSIFICATION:  
   NAME: Stewart, Michael I  
   REFERENCE/DOCKET NUMBER: 24-973  
 TELECOMMUNICATION INFORMATION:  
   TELEPHONE: (416) 595-1155  
 INFORMATION FOR SEQ ID NO: 3:  
   SEQUENCE CHARACTERISTICS:  
     LENGTH: 1992 amino acids  
     TYPE: amino acid  
     STRANEDNESS: single  
     TOPOLOGY: linear  
 US-10-175-282-3

Query Match    8.3%: Score 97; DB 8; Length 1992;  
 Best Local Similarity 22.8%; Pred. No. 23;  
 Matches 50; Conservative 40; Mismatches 93; Indels 36; Gaps 7;

Qy    13 SSDVNYSEIYQVAPQVNQALTAKYFGAIDGSTLRFDEKALQIAN----- 61  
 Db    1057 SHDAVTGGKIVDLKTELENKISSTAKTAQNSLHEFSVDAEQNNFTVSNPSSYDTSKTS 1116  
 Qy    62 DIPQAAVNTLNQTVQGTVQVSMIDKIVDIMK-----NVLSIVIDNKKWDQVTAII 115  
 Db    1117 DVITPAGENGITTKVNGKVVRGIDQTKGLTPKLTVGNNGKGIVIDSQNGQTIT-GL 1175  
 Qy    116 TNTFTNLNSQSEAWIIFYKEDAHKTSYNNILFAIQDEE---TGGYMATLPIAFDISVD 172  
 Db    1176 SNTLANTVNDGSV-----RTEQGNI---IKDEDKTRAASIVDVLISAGFNQGN 1222  
 Qy    173 IEKEKVLFTIKTDENYAVTVKAINVVAQALQSSRSKVV 211  
 Db    1223 -GEAVDFVSTYDVTNFADGNATTAKTYDDTSKTSKVV 1259

RESULT 11  
 US-10-175-275-3

Query Match    8.3%: Score 97; DB 8; Length 1992;  
 Best Local Similarity 22.8%; Pred. No. 23;  
 Matches 50; Conservative 40; Mismatches 93; Indels 36; Gaps 7;

Qy    13 SSDVNYSEIYQVAPQVNQALTAKYFGAIDGSTLRFDEKALQIAN----- 61  
 Db    1057 SHDAVTGGKIVDLKTELENKISSTAKTAQNSLHEFSVDAEQNNFTVSNPSSYDTSKTS 1116  
 Qy    62 DIPQAAVNTLNQTVQGTVQVSMIDKIVDIMK-----NVLSIVIDNKKWDQVTAII 115  
 Db    1117 DVITPAGENGITTKVNGKVVRGIDQTKGLTPKLTVGNNGKGIVIDSQNGQTIT-GL 1175  
 Qy    116 TNTFTNLNSQSEAWIIFYKEDAHKTSYNNILFAIQDEE---TGGYMATLPIAFDISVD 172  
 Db    1176 SNTLANTVNDGSV-----RTEQGNI---IKDEDKTRAASIVDVLISAGFNQGN 1222  
 Qy    173 IEKEKVLFTIKTDENYAVTVKAINVVAQALQSSRSKVV 211  
 Db    1223 -GEAVDFVSTYDVTNFADGNATTAKTYDDTSKTSKVV 1259

RESULT 10  
 US-10-175-282-3

Query Match    8.3%: Score 97; DB 8; Length 1992;  
 Best Local Similarity 22.8%; Pred. No. 23;  
 Matches 50; Conservative 40; Mismatches 93; Indels 36; Gaps 7;

Qy    13 SSDVNYSEIYQVAPQVNQALTAKYFGAIDGSTLRFDEKALQIAN----- 61  
 Db    1057 SHDAVTGGKIVDLKTELENKISSTAKTAQNSLHEFSVDAEQNNFTVSNPSSYDTSKTS 1116  
 Qy    62 DIPQAAVNTLNQTVQGTVQVSMIDKIVDIMK-----NVLSIVIDNKKWDQVTAII 115  
 Db    1117 DVITPAGENGITTKVNGKVVRGIDQTKGLTPKLTVGNNGKGIVIDSQNGQTIT-GL 1175  
 Qy    116 TNTFTNLNSQSEAWIIFYKEDAHKTSYNNILFAIQDEE---TGGYMATLPIAFDISVD 172  
 Db    1176 SNTLANTVNDGSV-----RTEQGNI---IKDEDKTRAASIVDVLISAGFNQGN 1222

Software: PatentIn Ver. 2.1  
 Seq ID No 3  
 Length: 1992  
 Type: PRT

Qy	173	I E K E K V L F P T I K O P E N Y A V T K A I N V Q A L Q S S R S K V V 1223 - G B A V D F V S T Y D T V N P A D G N A T A K V T Y D D T S K V V 1259	RESULT 12 US-10-282-122A-63417
Qy	63417	Sequence 63417, Application US/10282122A Publication No. US20040023129A1	Sequence 63417, Application US/10282122A Publication No. US20040023129A1
Db		GENERAL INFORMATION: APPLICANT: Wang, Liangshu APPLICANT: Zantudio, Carlos APPLICANT: Malone, Cheryl APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari APPLICANT: Zyskind, Judith APPLICANT: Wall, Daniel APPLICANT: Trawick, John APPLICANT: Carr, Grant APPLICANT: Yamamoto, Robert APPLICANT: Forsyth, R. APPLICANT: Xu, H.	GENERAL INFORMATION: APPLICANT: Wang, Liangshu APPLICANT: Zantudio, Carlos APPLICANT: Malone, Cheryl APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari APPLICANT: Zyskind, Judith APPLICANT: Wall, Daniel APPLICANT: Trawick, John APPLICANT: Carr, Grant APPLICANT: Yamamoto, Robert APPLICANT: Forsyth, R. APPLICANT: Xu, H.
Qy		TITLE OF INVENTION: Identification of Essential Genes in FILE REFERENCE: ELITA.034A	TITLE OF INVENTION: Identification of Essential Genes in FILE REFERENCE: ELITA.034A
Db		CURRENT APPLICATION NUMBER: US/10/282,122A CURRENT FILING DATE: 2003-02-20 PRIOR APPLICATION NUMBER: 60/191,078	CURRENT APPLICATION NUMBER: US/10/282,122A CURRENT FILING DATE: 2003-02-20 PRIOR APPLICATION NUMBER: 60/191,078
Qy		PRIOR FILING DATE: 2000-03-21 PRIOR APPLICATION NUMBER: 60/206,848	PRIOR FILING DATE: 2000-03-21 PRIOR APPLICATION NUMBER: 60/206,848
Db		PRIOR FILING DATE: 2000-05-23 PRIOR APPLICATION NUMBER: 60/207,727	PRIOR FILING DATE: 2000-05-23 PRIOR APPLICATION NUMBER: 60/207,727
Qy		PRIOR FILING DATE: 2000-05-26 PRIOR APPLICATION NUMBER: 60/230,335	PRIOR FILING DATE: 2000-05-26 PRIOR APPLICATION NUMBER: 60/230,335
Db		PRIOR FILING DATE: 2000-09-06 PRIOR APPLICATION NUMBER: 60/230,347	PRIOR FILING DATE: 2000-09-06 PRIOR APPLICATION NUMBER: 60/230,347
Qy		PRIOR FILING DATE: 2000-12-09 PRIOR APPLICATION NUMBER: 60/242,578	PRIOR FILING DATE: 2000-12-09 PRIOR APPLICATION NUMBER: 60/242,578
Db		PRIOR FILING DATE: 2001-10-23 PRIOR APPLICATION NUMBER: 60/253,625	PRIOR FILING DATE: 2001-10-23 PRIOR APPLICATION NUMBER: 60/253,625
Qy		PRIOR FILING DATE: 2000-11-27 PRIOR APPLICATION NUMBER: 60/257,931	PRIOR FILING DATE: 2000-11-27 PRIOR APPLICATION NUMBER: 60/257,931
Db		PRIOR FILING DATE: 2000-12-22 PRIOR APPLICATION NUMBER: 60/267,636	PRIOR FILING DATE: 2000-12-22 PRIOR APPLICATION NUMBER: 60/267,636
Qy		PRIOR FILING DATE: 2001-02-09 PRIOR APPLICATION NUMBER: 60/269,308	PRIOR FILING DATE: 2001-02-09 PRIOR APPLICATION NUMBER: 60/269,308
Db		Remaining Prior Application data removed - See File Wrap NUMBER OF SEQ ID RNS: 78614 SOFTWARE: PatentIn version 3.1 SEQ ID NO 63417 LENGTH: 421 TYPE: PRT	Remaining Prior Application data removed - See File Wrap NUMBER OF SEQ ID RNS: 78614 SOFTWARE: PatentIn version 3.1 SEQ ID NO 63417 LENGTH: 421 TYPE: PRT
Qy		ORGANISM: Mycoplasma genitalium US-10-282-122A-63417	ORGANISM: Mycoplasma genitalium US-10-282-122A-63417
Db		Query Match 8.2%; Score 95.5; DB 15; Length 17 Best Local Similarity 23.6%; Pred. No. 3.8; Matches 48; Conservative 41; Mismatches 75; Indeed 17	Query Match 8.2%; Score 95.5; DB 15; Length 17 Best Local Similarity 23.6%; Pred. No. 3.8; Matches 48; Conservative 41; Mismatches 75; Indeed 17
Db		17 V N S T T Y O V A P Q Y N Q A L T L A K Y P Q G A T D S T R P D F E K A L Q I A N 233 V K L S D M N Q V L Q K A V G V N V E V N E --AV--N P F Q Q D L Q V Q D Q F V Qy	17 V N S T T Y O V A P Q Y N Q A L T L A K Y P Q G A T D S T R P D F E K A L Q I A N 233 V K L S D M N Q V L Q K A V G V N V E V N E --AV--N P F Q Q D L Q V Q D Q F V
Qy		77 Q Q G T V Q V S V M I D K I V D I M Q N V L S I V D N Q K F W D Q V T A A T T N T F T N 287 Q A K T R Q -----K A L E J Y Q D V L T -----S K C A W N R F L S F I -----	77 Q Q G T V Q V S V M I D K I V D I M Q N V L S I V D N Q K F W D Q V T A A T T N T F T N 287 Q A K T R Q -----K A L E J Y Q D V L T -----S K C A W N R F L S F I -----
Db		137 D A H K T S Y Y N I L F A I Q D E T G G M A T L I P A F - D I S V D I E K E K V - 330 G F F P K P K Y -----K A S K I K A E S G L I U F F D E D L A K G I N I L G A R M K C K K	137 D A H K T S Y Y N I L F A I Q D E T G G M A T L I P A F - D I S V D I E K E K V - 330 G F F P K P K Y -----K A S K I K A E S G L I U F F D E D L A K G I N I L G A R M K C K K
Qy		185 D T E Y A Y T V R A I N V V A L O S S R D 207	185 D T E Y A Y T V R A I N V V A L O S S R D 207

RESULT 13  
 US-10-282-122A-73861  
 Sequence 73861, Application US/10282122  
 Publication No. US20060229129A1  
 GENERAL INFORMATION:  
 i APPLICANT: Wang, Liangsu  
 i APPLICANT: Zamudio, Carlos  
 i APPLICANT: Malone, Cheryl  
 i APPLICANT: Haselbeck, Robert  
 i APPLICANT: Ohlsen, Kari  
 i APPLICANT: Zyskind, Judith  
 i APPLICANT: Wall, Daniel  
 i APPLICANT: Trawick, John  
 i APPLICANT: Carr, Grant  
 i APPLICANT: Yamamoto, Robert  
 i APPLICANT: Forsyth, R.  
 i APPLICANT: Xu, H.  
 i TITLE OF INVENTION: Identification of  
 i FILE REFERENCE: ELITA.034A  
 i CURRENT APPLICATION NUMBER: US/10/282,  
 i CURRENT FILING DATE: 2003-02-20  
 i PRIOR APPLICATION NUMBER: 60/151,078  
 i PRIOR FILING DATE: 2000-03-21  
 i PRIOR APPLICATION NUMBER: 60/206,848  
 i PRIOR FILING DATE: 2000-05-23  
 i PRIOR APPLICATION NUMBER: 60/207,727  
 i PRIOR FILING DATE: 2000-05-26  
 i PRIOR APPLICATION NUMBER: 60/230,335  
 i PRIOR FILING DATE: 2000-09-06  
 i PRIOR APPLICATION NUMBER: 60/230,347  
 i PRIOR FILING DATE: 2000-09-09  
 i PRIOR APPLICATION NUMBER: 60/242,578  
 i PRIOR FILING DATE: 2000-10-23  
 i PRIOR APPLICATION NUMBER: 60/253,625  
 i PRIOR FILING DATE: 2000-11-27  
 i PRIOR APPLICATION NUMBER: 60/257,931  
 i PRIOR FILING DATE: 2000-12-22  
 i PRIOR APPLICATION NUMBER: 60/267,636  
 i PRIOR FILING DATE: 2001-02-09  
 i PRIOR APPLICATION NUMBER: 60/269,308  
 i PRIOR FILING DATE: 2001-02-16  
 i Remaining Prior Application data removed  
 i NUMBER OF SEQ ID NOS: 78614  
 i SOFTWARE: PatentIn version 3.1  
 i SEQ ID NO: 73861  
 i LENGTH: 1876  
 i TYPE: PRT  
 i ORGANISM: Streptococcus pneumoniae  
 i US-10-282-122A-73861

Query Match 7 ITILVPSDGVNNVSRIYQVAPQVYQVNAQ Score 9  
 Best Local Similarity 20.4% Pred. N  
 Matches 46 Conservatory 41; Misam

Qy	7 ITILVPSDGVNNVSRIYQVAPQVYQVNAQ
Db	553 ICKLAIKDKGQSVLKV-TVAYENNLNAT
Qy	59 IANDIPOQAVVN-----TNTQTVQGTT
Db	612 IQLDKKKVEIKNIKETSLMNNDAEQEY
Qy	96 NVLSITVDNPKFWDFQVTAATNTTFNLL
Db	672 SVEEVVVDGKTLYKVAAKADPLVQRRA
Qy	155 ETGGWMAATLPPIAFDI-SVDFBKEKVLF
Db	732 Q-ANPGBEFKUGADINAVNVKPGAKY

RESULT 14  
US-10-369-493-17326  
Sequence 17326, Application US/10369493  
GENERAL INFORMATION  
APPLICANT: Cao, Yongwei  
APPLICANT: Hinkle, Gregory J.  
APPLICANT: Slater, Steven C.  
APPLICANT: Goldmar, Barry S.  
APPLICANT: Chen, Xianfang  
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF PLANTS WITH IMPROVED PROPERTIES  
FILE REFERENCE: 38-10(52052) B  
CURRENT APPLICATION NUMBER: US/10/369, 493  
CURRENT FILING DATE: 2003-02-28  
PRIOR APPLICATION NUMBER: US 60/360, 039  
PRIOR FILING DATE: 2002-02-21  
NUMBER OF SEQ ID NOS: 47374  
SEQ ID NO 17326  
LENGTH: 249  
TYPE: PRT  
ORGANISM: *Bacillus halodurans*  
us-10-369-493-17326

Query Match Score 8.1%; Best Local Similarity 21.0%; Pred. No. 2,3; Mismatches 38; Indels 37; Gaps 7;  
Matches 37; Conservative 38;

Qy 62 DIPQAAVNTLNQTVQGQTQVQSVMI -----DKIVDIMKVLISIVDNKKFWDQVTAII 115  
Db 8 DVGKVPRPHNDTNGTIMEKGQLVVVADGMGGHQAGDVASKWATELL--KEAWBEAS-- 62

Qy 116 TNTFTNINQSSEAWITYKEDAHKTYYNTLFAOTDEETGVMATLPIAFDISYDEK 175  
Db 63 ---LSPSQSEGWLNRQHNESLHY---AQKHEECGGMGTIL---VAIVDK 109

Qy 176 EKVLFPTIKDTENYAVTVKAINVVOAQLQSSRDSKVUDAF-----KSPRHLPRK 223  
Db 110 ERVTIAHIGDSRAYLINEHGFPS-----QKTRDHSLVNLVRGQISDEAHHPRK 160

RESULT 15  
US-10-424-599-217207  
Sequence 217207, Application US/10424599  
GENERAL INFORMATION  
APPLICANT: La Rosa, Thomas J  
APPLICANT: Kovacic, David K  
APPLICANT: Zhou, Yihua  
APPLICANT: Cao, Yongwei  
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
FILE REFERENCE: 38-21(53223) B  
CURRENT APPLICATION NUMBER: US/10/424, 599  
CURRENT FILING DATE: 2003-04-28  
NUMBER OF SEQ ID NOS: 285684  
SEQ ID NO 217207  
LENGTH: 356  
TYPE: PRT  
FEATURE: Glycine max  
OTHER INFORMATION: Clone ID: PAT\_MRT3847\_38165C.1.dep

RESULT 16  
US-10-424-599-217207  
Query Match Score 8.1%; Best Local Similarity 20.7%; Pred. No. 3,7; Mismatches 39; Indels 114; Gaps 10;  
Matches 58; Conservative 39;

Qy 5 RVITLTVPSSDV-----VRYSEIYQVAPOYVQNQTLAKYF----- 40  
Db 74 RALITTAEKNIPWRAKMAQEILESEVTELESIONOSLVYPDYLNPFAYERGLNLTLWL 133

RESULT 14  
US-10-369-493-17326  
Sequence 17326, Application US/10369493  
GENERAL INFORMATION  
APPLICANT: Cao, Yongwei  
APPLICANT: Hinkle, Gregory J.  
APPLICANT: Slater, Steven C.  
APPLICANT: Goldmar, Barry S.  
APPLICANT: Chen, Xianfang  
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF PLANTS WITH IMPROVED PROPERTIES  
FILE REFERENCE: 38-10(52052) B  
CURRENT APPLICATION NUMBER: US/10/369, 493  
CURRENT FILING DATE: 2003-02-28  
PRIOR APPLICATION NUMBER: US 60/360, 039  
PRIOR FILING DATE: 2002-02-21  
NUMBER OF SEQ ID NOS: 47374  
SEQ ID NO 17326  
LENGTH: 249  
TYPE: PRT  
ORGANISM: *Bacillus halodurans*  
us-10-369-493-17326

Query Match Score 94.5%; Best Local Similarity 21.0%; Pred. No. 1,1; Mismatches 1; Indels 1; Gaps 1;  
Matches 134; Conservative 134;

Qy 95 KNVLSIVIDNKKFWDQV-TAAT-----NTPTNLNSQESE-----AWIFYKEDA- 138  
Db 191 -GCSCVGISTRLAKDKEPTAKVTKGFMNISYFYAWNQQKQERAMPKEPKWTHANGEDPTV 248  
Qy 139 -HKTSYYNILPQDQET-----GGVMMATLPIAFDISYDEKRYLFL 180  
Db 249 LPSKSFELIVSIAFLHBCPTRVIVNLVREAFLRPGSTLALTDFSLSKVLOBLSPVLF 308

Qy 181 VRIKDTENYAVTVKAINVVOAQLQSSRDSKVUDAFKSPRHL 220  
Db 309 TLVKSTBPFIDEXYLTDETIREAGFVNITSILTDPHV 348

Search completed: June 26, 2005, 16:09:50  
Job time : 160 secs

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Run on:	June 26, 2005, 15:47:02 ;	Search time	162 Seconds (without alignments)		
		551.492 Million cell updates/sec			
Title:	US-10-767-605-2				
Perfect score:	1165				
Sequence:	MFPMJRVITLTVPSDVVNTS.....DAFKSPRHLPLRKHKICNS	231			
Scoring table:	BLOSUM62				
	Gapop 10.0 , Gapext 0.5				
Searched:	2105692 seqs,	386760381 residues			
Total number of hits satisfying chosen parameters:	2105692				
Minimum DB seq length:	0				
Maximum DB seq length:	2000000000				
Post-processing:	Minimum Match 0% Maximum Match 100%				
	Listing first 45 summaries				
Database :	A_Geneseq_16Dec04:*				
	1: geneseqP19808:*				
	2: geneseqP19908:*				
	3: geneseqP20008:*				
	4: geneseqP20018:*				
	5: geneseqP20028:*				
	6: geneseqP20038:*				
	7: geneseqP2003bs:*				
	8: geneseqP20048:*				
Pred. No.	is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.				
		SUMMARIES			
Result No.	Score	Query Match	Length	DB ID	Description
1	1151	98.8	231	AAW55027	Bacillus thuringiensis CryET29 crystal protein - having activity against the Southern corn rootworm, Western corn rootworm, Colorado potato beetle, Japanese beetle and red flour beetle and also against fleas, in particular larvae of the cat flea, Ctenocephalides felis. CryET29 can therefore be used to prevent infestations by these insects. The gene can be used to produce transgenic plants which express the toxic proteins and therefor insecticidal activity against pests.
2	457	39.2	249	AAAR10282	Bacillus thuringiensis Mutant 27
3	456	39.1	249	AAAR04831	Bacillus thuringiensis Mutant 27
4	451	38.7	249	AAAR10853	Bacillus thuringiensis Mutant 27
5	450	38.6	249	AAAR10283	Bacillus thuringiensis Mutant 27
6	450	38.6	249	AAAR10309	Bacillus thuringiensis Mutant 27
7	442	38.0	220	AAAR24023	Bacillus thuringiensis Anticancer Peptide
8	424	36.4	218	AAAPB0062	Bacillus thuringiensis Peptide
9	423	36.4	265	AAAR70754	Bacillus thuringiensis Delta-endotoxin
10	411	36.4	265	AAAR1966	Bacillus thuringiensis Delta-endotoxin
11	433	36.4	265	AAAN07850	Bacillus thuringiensis Delta-endotoxin
12	422	36.4	265	AAAY01207	Bacillus thuringiensis Delta-endotoxin
13	417	35.8	222	AAAR10755	Bacillus thuringiensis Delta-endotoxin
14	417	35.8	222	AAAS91967	Bacillus thuringiensis Truncated Peptide
15	417	35.8	222	AAAY01208	Bacillus thuringiensis Truncated Peptide
16	415	35.7	265	AAAB03646	Bacillus thuringiensis Truncated Peptide
17	103	8.8	401	ABU51322	Bacillus thuringiensis Truncated Peptide
18	103	8.8	415	ABU52179	Bacillus thuringiensis Truncated Peptide
19	101	8.7	477	AAV10993	Bacillus thuringiensis Truncated Peptide
20	100	8.6	210	ABU51679	Bacillus thuringiensis Truncated Peptide
21	97	8.3	1992	AAAN04505	Bacillus thuringiensis Truncated Peptide
22	97	8.3	1992	AAAB69137	Bacillus thuringiensis Truncated Peptide
23	97	8.3	1992	AAAB69133	Bacillus thuringiensis Truncated Peptide
24	97	8.3	2047	AAAB69134	Bacillus thuringiensis Truncated Peptide
25	96.5	8.3	201	AAAB59843	Bacillus thuringiensis Truncated Peptide
				Sequence 231 AA;	
				Query Match	98.8%; Score 1151; DB 2; Length 231;





PN	US000875-H.	XX	XX	DR	WPI; 1992-190107/23.
PD	01-JAN-1991.	XX	XX	PT	Anticancer agent for thermo-chemotherapy - contains polypeptide produced from bacillus, and is pref. used with phloemycin.
PF	18-MAR-1988;	88US-00170211.	XX	PT	
XX			XX		
PR	18-MAR-1988;	88US-00170211.	XX	PS	
XX			XX		
PA	(DUPO ) DU PONT DE NEMOURS & CO E I.	XX	XX		
XX			CC		
PI	Ellar DJ, Ward ES;	XX	CC		
DR	WPI; 1991-028850/04.	XX	CC		
XX			CC		
PT	Nucleic acid fragments encoding mutant 27 KD delta endotoxins - from Bacillus thuringiensis var. Israeliensis, have improved insecticidal properties, part. against mosquitoes.	XX	CC		
PS	Disclosure; Fig 1; 5pp; Japanese.	XX	CC		
XX			CC		
CC	This mutant 27 KD delta endotoxin has a single amino acid substitution (Lys-124 to Ala) in the wild-type sequence. This results in a soluble insecticidal protein with improved insecticidal properties, e.g. lower haemolytic activity and greater expression in cells contg. sig. amts. of phosphatidate-type toxin receptors. It is hence useful e.g. against mosquitoes. See also AARI0853 and AARI0282-83	XX	CC		
SQ	Sequence 249 AA;	XX	CC		
Query	5 RVTILTVPS-SDVVNTSEIYQV-APOVNQALTLAKYFOGAI-----DGSLRDFEKA	56	5		
Db	25 RVTILRVEDPNEINNLLSINEIDNPNTYQLDMLANAQNVLVPTSTDGFDALRSPMKG	84			
Query	57 LOIANDI-PQAVVNTLNQTYQGTIVQVSIMDKIVDIMKNVLSTIVDNKFWFDQYTAII	115		RESULT 8	
Db	85 LEIANTITPMGAVVSTDQNTQTNNQSVWNINKVLELVATLGVALSGSVI-DOLTAIV	143		ID AAP90062	
Query	116 TNTFTNLNSQSEAMWIFPYKEDAHKTISYYNNILFAQDDETGGMATLPIAFDISVIEK	175		ID AAP90062;	
Db	144 TNTFTNLNTQNEAWIFWGKETANQNTNYTNVLFAQNAQTGQGNYXCVPGFELKVSAVK	203		AC	
Query	176 EKVLFTTIKDOPENAYVTKAINVQALQSSRSDSKVVD	212		XX	DT 24-OCT-2003 (revised)
Db	204 EQVLFPTIQDQSASVNVNIQSLKFAQPLVSSSTQYPIAD	240		DT 25-MAR-2003 (revised)	
				DT 09-AUG-1990 (first entry)	
				XX	
				XX	Peptide with anticancer activity.
				XX	
				KW	Anticancer agent; enhancer.
				XX	
				OS	Bacillus thuringiensis serovar israelensis; ONR-60A.
				XX	
				PN	JP0104019-A.
				XX	
				PD	21-APR-1989.
				XX	
				PF	29-JUL-1988;
				XX	88JP-00108207.
				PR	31-JUL-1987;
				XX	87JP-0010347.
				PA	(TOAG ) TOA GOSEI CHEM IND LTD.
				XX	
				DR	WPI; 1989-161673/22.
				XX	
				XX	Anticancer agents - contain polypeptide enhancer produced by Bacillus microorganism.
				XX	
				PS	Claim 1; Fig 6; 7pp; Japanese.
				XX	
				CC	The polypeptide has anticancer activity and is capable of synergistically enhancing other agents such as bisomycin, adriamycin, 5-FU and esp. neocarzinostatin and thio-TEP. See also J01104018. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 24-OCT-2003 to standardise OS
				CC	
				CC	
				PA	
				PA	(TOAG ) TOA GOSEI CHEM IND LTD.

CC	field	XX	Sequence 265 AA;
SQ	Sequence 218 AA;	Query Match 36.4%; Score 424; DB 1; Length 218; Best Local Similarity 44.8%; Pred. No. 7.5e-33; Mismatches 90; Conservative Matches 90;	Score 423.5; DB 2; Length 265; Best Local Similarity 40.9%; Pred. No. 1.1e-32; Mismatches 47; Conservative Matches 94; Indels 10; Gaps 5;
Qy	14 SDVNVNSYYIYQV-APOVNQALTLAKYFQGAI-----DGSTLRLRDPBKAQJANDI-PQ 65	Qy 5 RVTILTRPVSSDVNYSBIVQVA---PQYVNQALTLAKYFQGAI-----DGSTLRLRDFE 54	
Db	6 NEINNLISINEIDNPNTYLQAIMLANAFNALVPTSTDFGDLRFSMPKGLEIAINTITPQ 65	Db 38 RVIYKV--KDPDTTQLLEIBENPNVYVQAIIQAAAQFDALVPTETEGEARFSMP 95	
Qy	66 AAVVNTLNQTVGGTGVQVSMIDKIVDINKNLNSIVIDNKFKWQVTA 113	Qy 55 KALQIANDI-POAAVNTLNQTVGGTGVQVSMIDKIVDINKNLNSIVIDNKFKWQVTA 113	
Db	66 GAVSVSYVHVTQTNN-QVSWMINKVLETLKTVLGVALGSVT-DQLTAVINFINLTQ 123	Db 96 KGLEVAKTIQPKGAVVAYTDQTLSQSNNOVSVMDRVISVLKTMGVALSG-SITQLTA 154	
Qy	126 ESEAWIPIFYKEDAHKTSYYNNILFAIQDEETGSMATLPIADISVDIEKEKVLFTYKD 185	Qy 114 AITNTFTNLNQSEAWIPIFYKEDAHKTSYYNNILFAIQDEETGSMATLPIADISVDI 173	
Db	124 KNEAWIPIFGKETANOTNTYNTVNLFAINAQQTGGMXCVPGFEIKYSAVEQVLFFTIQD 183	Db 155 AITDTFTNLNQFDSAWVFMKGKETSHQNTNTVNMFAIQNETTGRYMMCVPGFBIRVFT 214	
Qy	186 TENAVTAKAINVQALQSSR 206	Qy 174 EKEKVLFTVTKDTEAVTAKAINVQALQSSRDSKVVD--AFKSPRHL 220	
Db	184 SASVNTNIQSLKPAQPLVSSQ 204	Db 215 DKRTVLFLLTQDYANTSVNITGLRRAQPLTDSRALAINDISEARLSSSKYL 264	
RESULT 9			
ID	AAR70754	XX	AAR91966 standard; protein; 265 AA.
AC	AAR70754;	XX	AAR91966;
XX	16-OCT-2003 (revised)	XX	16-OCT-2003 (revised)
DT	25-MAR-2003 (revised)	DT	25-MAR-2003 (revised)
DT	15-AUG-1995 (first entry)	DT	18-JUL-1996 (first entry)
XX	Delta-endotoxin 201T6.	XX	PS201T6 30 kDa toxin.
DB	KW Delta-endotoxin: crystal protein; insecticide; pesticide; biological control agent; pest control; yellow fever mosquito; Aedes aegypti; housefly; Musca domestica; leatmining fly; Liriomyza trifolii; Western corn rootworm; Diabrotica virgifera; dipteran insect.	XX	Toxin; bacillus thuringiensis; isolate PS201T6.
OS	Bacillus thuringiensis; var. neoleoensis.	XX	Bacillus thuringiensis; isolate PS201T6.
XX	PN WO9502693-A1.	XX	OS Bacillus thuringiensis; isolate PS201T6.
XX	PD 26-JAN-1995.	XX	XX
PP	14-JUL-1994; 94WO-US007887.	PP	06-FEB-1996.
XX	(MYCO ) MYCOGEN CORP.	XX	XX
PI	Payne J., Narva KB., Uyeda KA., Stalder CJ., Michaels TB;	PI	30-SEP-1993; 93US-00129609.
PR	WPI: 1995-067337/09.	XX	PR 06-NOV-1991; 91US-00708654.
DR	DR DR N-PSDB; AA085261.	XX	PR 19-OCT-1992; 92US-00938551.
XX	PR 30-SEP-1993; 93US-00129610.	XX	DR N-PSDB; AAT16027.
PA	(MYCO ) MYCOGEN CORP.	PA	XX
XX	PT New purified toxin active against cockroaches - produced by a culture of Bacillus thuringiensis isolate PS201T6, has a mol. wt. less than 31 kD.	PT	PT New purified toxin active against cockroaches - produced by a culture of Bacillus thuringiensis isolate PS201T6, has a mol. wt. less than 31 kD.
PS	XX Example 3; Col 17-20; 12pp; English.	XX	XX Example 3; Col 17-20; 12pp; English.
XX	CC This sequence represents the 30 kDa Bacillus thuringiensis (B.t.) toxin, which is active against cockroaches. The encoding sequence was obtained CC from the B.t. isolate PS201T6, using the primers represented by AAT16031 CC and AAT16032. The toxin has a high activity against cockroaches while CC not affecting humans or animals. Insecticides such as this can be safely CC used in homes and restaurants. These insecticides will also be effective CC against strains resistant to currently used insecticides. The B.t. CC isolate PS201T6 may also be used directly to control the cockroaches. CC (Updated on 25-MAR-2003 to correct PP field.) (Updated on 16-OCT-2003 to CC standardise OS field)	CC	CC This sequence represents the 30 kDa Bacillus thuringiensis (B.t.) toxin, which is active against cockroaches. The encoding sequence was obtained CC from the B.t. isolate PS201T6, using the primers represented by AAT16031 CC and AAT16032. The toxin has a high activity against cockroaches while CC not affecting humans or animals. Insecticides such as this can be safely CC used in homes and restaurants. These insecticides will also be effective CC against strains resistant to currently used insecticides. The B.t. CC isolate PS201T6 may also be used directly to control the cockroaches. CC (Updated on 25-MAR-2003 to correct PP field.) (Updated on 16-OCT-2003 to CC standardise OS field)
SQ	Sequence 265 AA;	XX	Sequence 265 AA;



a *Bacillus thuringiensis* delta-endotoxin from *B. thuringiensis* isolate PS123D1, deposited in NRRL B-21011. The hemipteran insect pests that can be controlled by the method are specifically Lygus hesperus and Lygus lineolaris. The method provides an alternative to control of hemipteran pests with chemical pesticides, allowing more environmentally friendly insect management and provides a tool for management of insecticide resistance. The present sequence represents an approximately 30kD delta-endotoxin of *B. thuringiensis* isolate PS201T6. (Updated on 20-MAR-2003 to correct PF field.)

XX Sequence 265 AA;

Query Match	36.4%	Score 423.5;	DB 2;	Length 265;
Best Local Similarity	40.9%	Pred. No. 1.1e-32;		
Matches	94;	Mismatches	47;	Indels 17; Gaps 6;

Qy 5 RVTITLTVPSDDVNVYSEIYQVA---POVNQNLTLAKYFOGAI----DGSTLRFPEKALQ1ANDI-PQA 66  
Db 38 RVTYLKV-KDPIDTTQLEITBTRIENPVYLVQLAQAAFDQALVPTEFGBAIRSPMP 95  
Qy 55 KALQIANDI-PQAVAVNTLNQTVQGGTVQVSWMIDKTVUDIMKVLNSIVIDNKKFWDQVTA 113  
Db 96 KGLEVAKTIQPKGAVVAYTDQTSQSNNQVSYMSIDRVTSVSLKTVMGVLSG-SITPOLTA 154  
Qy 114 AITDTFTLNSOSEAWTFYYKEQDAHKTSYYNNILFAQDEETGGMATAFLPIAFDISVDI 173  
Db 155 AITDTFTLNTQKDSAWFWGETSHQNYTNVMPAQNETHGRVMCVPGFERKFT 214  
Qy 174 EKEKVLFTTIKOTENYAVTKVAINVQVALQSSRDSKVVD---AFKSPRHL 220  
Db 215 DKGRTVLFITKTDYANYSYNSNIQTLRFAQPLIDSRLSINDLSEALRSSKL 264

## RESULT 13

AAR70755 standard; protein, 222 AA.

XX AAR70755;  
XX DT 16-OCT-2003 (revised)  
DT 25-MAR-2003 (revised)  
DT 15-AUG-1995 (first entry)  
XX DE Delta-endotoxin 201T6 truncation.  
XX Delta-endotoxin; crystal protein; insecticide; Pesticide; Biological control agent; pest control; yellow fever mosquito; Aedes aegypti; housefly; Musca domestica; leafmining fly; Liriomyza trifolii; Western corn rootworm; Diabrotica virgifera; dipteran insect.  
XX OS *Bacillus thuringiensis*; var. neoleoensis.  
XX WO9502693-A1.  
PN 26-JAN-1995.  
XX PP 14-JUL-1994; 94WO-US007887.  
XX PR 15-JUL-1993; 93US-00093199.  
PR 30-SEP-1993; 93US-00129610.  
PA (MYCO ) MYCOGEN CORP.

XX Payne J., Narva KE, Uyeda KA, Staider CJ, Michaela TE;  
DR WPI; 1995-067337/09.  
DR N-PSDB; AAQ85261.

XX Delta endotoxins produced by *Bacillus thuringiensis* isolates - are active against dipteran and/or corn rootworm.

XX Claim 5; Page 33-34; 38pp; English.

## XX

DNA encoding a novel 30 kDa delta-endotoxin, 201T6 toxin, was isolated from a gene library of *Bacillus thuringiensis* PS01T6 (NRRL B-18750) in lambda Gem-11. Removal of the 43 N-terminal amino acids of the toxin gave a 25 kD toxin (AAR70755) of increased scope and potency. Recombinant hosts expressing the toxin gene are used for biological control of insect pests. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 16-OCT-2003 to standardise OS field)

## XX

Sequence 222 AA;

Query	35.8%	Score 417;	DB 2;	Length 222;
Match	41.9%	Pred. No. 3.7e-32;		
Best Local Similarity	41.9%	Mismatches	42;	Indels 12; Gaps 5;
Matches	91;	Conservative	42;	

Qy 15 DVNVYSEIYQVA-PQVNQNLTLAKYFOGAI----DGSTLRFPEKALQ1ANDI-PQA 66  
Db 6 DTQOLLETETEINPVYLVQIAAAFDQALVPTEFGEAIRFSMPKGLEYARTIQPKG 65  
Qy 67 AVNTLNQTVQGGTVQSVMDKVIDMKVNLISIVIDNKKFWDQVTA 126  
Db 66 AVVAYTQTLQSNNNQVSVMDRIVISVLTQTMGVALS-G-SITQLTAAITDFTNLNTQK 124  
Qy 127 SAWIIFTYKEDDAHKTSYNNILFAQDPBTGVMATPIAFDISVDPIDBKEKYLFTVLTQDT 186  
Db 125 DSAWFNGKEISHTQNTTYNNMPAQNBTGVRMCMVPIGFERVFDKRTVLPPLTKDY 184  
Qy 187 ENYAVTVAIAINVQVALQSSRDSKVVD---AFKSPRHL 220  
Db 185 ANYSVNQTLREAPLIDSRLSINDLSEALRSSKL 221

## RESULT 14

AAR91967

## XX

AC

AAR91967;

XX

DT

16-OCT-2003

(revised)

DT

25-MAR-2003

(first entry)

XX

DE

Truncated PS201T6 30 kDa toxin.

XX

KW

Toxin; *bacillus thuringiensis*; PS201T6; cockroach; insecticide.

OS

Bacillus thuringiensis; isolate PS201T6.

XX

PN

USS489432-A.

XX

PD

06-FEB-1996.

XX

PP

30-SEP-1993;

93US-00129609.

XX

PR

06-NOV-1991;

91US-00788654.

XX

PR

19-OCT-1992;

92US-00958551.

XX

PA

(MYCO ) MYCOGEN CORP.

XX

Schnepp HE,

Brower DO,

Kennedy MK,

Payne JM,

Randall JB;

XX

DR

WPI; 1996-115589/12.

N-PSDB;

AAT16027.

XX

PT

New purified toxin active against cockroaches - produced by a culture of

PT

*Bacillus thuringiensis* isolate PS201T6, has a mol. wt. less than 31 kD.

XX

Claim 1; Col 19-22; 12pp; English.

XX

This sequence represents a truncated form of the 30 kDa Bacillus

CC

thuringiensis (B.t.) toxin (see AAR91966), which is active against

CC

cockroaches. The encoding sequence was obtained from the B.C. isolate

CC

PS201T6, using the primers represented by AAT16031 and AAT16032. The

CC

toxin has a high activity against cockroaches, while not affecting humans or animals. Insecticides such as this can be safely used in homes and restaurants. These insecticides will also be effective against strains resistant to currently used insecticides. The B.t. isolate PS20176 may also be used directly to control the cockroaches. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 16-OCT-2003 to standardise OS field)

Sequence 222 AA;

```
Query Match 35.8%; Score 417; DB 2; Length 222;
Best Local Similarity 41.9%; Pred. No. 3.7e-32;
Matches 91; Conservative 42; Mismatches 72; Indels 12; Gaps 5;
Qy 15 DVVNVSEIXOVA-POVNQALTLAKYFOGAI-----DGSTLRFDFEKAQIANDI-PQA 66
Db 6 DTTQLEITIEENPVLYQLAQIAFQDALVPTTEFGFAIRSMMPKGLEVAKTIQPKG 65
Qy 67 AVVNTLNQTYQGGTQVSMSMIDKIVDMMKVLSIVDNKKFWQVTAATNTFTNLNSQE 126
Db 66 AVVAYTDQTLSQSNQSVSMDRVTSVLKTMGVLSG-SIITQDTAAATDFTNLNTQK 124
Qy 127 SBAWIFYYKEDAHKTSYYNNILFAIODEETGGVNMATLPIAFDISVIEKEKVLFTIKDT 186
Db 125 DSANYFWGKETSHQNYTNVMFAQNETIGRVNMCPVGPBIRVFTDKRTVLFLITKDY 184
Qy 187 ENYAVTVKAINVQALQSRSDSKVVD--AFKSPPHL 220
Db 185 ANYSYNIQTURFAQPLIDSRLSINDLSEALRSSKYL 221
```

RESULT 15  
ID AAY01208 standard: protein; 222 AA.

XX AAY01208;  
.AC XX DT 20-MAR-2003 (revised)  
XX 25-MAY-1999 (first entry)

DB *B. thuringiensis* PS20176 truncated delta-endotoxin.

KW Hemipteran; insect; pest: *Bacillus thuringiensis*; delta-endotoxin;  
KW *Lugus hesperus*; *Lugus lineolaris*; insecticide; chemical pesticide;  
XX insect management; insecticide resistance.

*Bacillus thuringiensis*.

PN US5885963-A.  
XX 23-MAR-1999.

XX PD 07-JUN-1996; 96US-00657579.  
XX PR 07-JUN-1995; 95US-00475924.  
XX PA (MYCO ) MYCOGEN CORP.  
XX PI Conlan C, Stockhoff B;  
XX DR WPI; 1999-228582/19.

XX New method of killing hemipteran insect pests - by administration of a  
PT *Bacillus thuringiensis* delta-endotoxin from *B. thuringiensis* isolate  
PR PS123D1, deposited in NRRL B-21011.  
XX Example: Col 17-18; 10pp; English.

XX The invention relates to killing hemipteran insect pests by administering  
CC a *Bacillus thuringiensis* delta-endotoxin from *B. thuringiensis* isolate  
CC PS123D1, deposited in NRRL B-21011. The hemipteran insect pests that can  
CC be controlled by the method are specifically *Lugus hesperus* and *Lugus*  
CC *lineolaris*. The method provides an alternative to control of hemipteran  
CC pests with chemical pesticides, allowing more environmentally-friendly

insect management and provides a tool for management of insecticide resistance. The present sequence represents a truncated delta-endotoxin of *B. thuringiensis* isolate PS20176 of about 25 kD. (Updated on 20-MAR-2003 to correct PF field.)

Sequence 222 AA;

```
Query Match 35.8%; Score 417; DB 2; Length 222;
Best Local Similarity 41.9%; Pred. No. 3.7e-32;
Matches 91; Conservative 42; Mismatches 72; Indels 12; Gaps 5;
Qy 15 DVVNVSEIXOVA-POVNQALTLAKYFOGAI-----DGSTLRFDFEKAQIANDI-PQA 66
Db 6 DTTQLEITIEENPVLYQLAQIAFQDALVPTTEFGFAIRSMMPKGLEVAKTIQPKG 65
Qy 67 AVVNTLNQTYQGGTQVSMSMIDKIVDMMKVLSIVDNKKFWQVTAATNTFTNLNSQE 126
Db 66 AVVAYTDQTLSQSNQSVSMDRVTSVLKTMGVLSG-SIITQDTAAATDFTNLNTQK 124
Qy 127 SBAWIFYYKEDAHKTSYYNNILFAIODEETGGVNMATLPIAFDISVIEKEKVLFTIKDT 186
Db 125 DSANYFWGKETSHQNYTNVMFAQNETIGRVNMCPVGPBIRVFTDKRTVLFLITKDY 184
Qy 187 ENYAVTVKAINVQALQSRSDSKVVD--AFKSPPHL 220
Db 185 ANYSYNIQTURFAQPLIDSRLSINDLSEALRSSKYL 221
```

Search completed: June 26, 2005, 16:02:31
 Job time : 164 SECs

CC insect management and provides a tool for management of insecticide  
CC resistance. The present sequence represents a truncated delta-endotoxin  
CC of *B. thuringiensis* isolate PS20176 of about 25 kD. (Updated on 20-MAR-  
CC 2003 to correct PF field.)

Sequence 222 AA;

```
Query Match 35.8%; Score 417; DB 2; Length 222;
Best Local Similarity 41.9%; Pred. No. 3.7e-32;
Matches 91; Conservative 42; Mismatches 72; Indels 12; Gaps 5;
Qy 15 DVVNVSEIXOVA-POVNQALTLAKYFOGAI-----DGSTLRFDFEKAQIANDI-PQA 66
Db 6 DTTQLEITIEENPVLYQLAQIAFQDALVPTTEFGFAIRSMMPKGLEVAKTIQPKG 65
Qy 67 AVVNTLNQTYQGGTQVSMSMIDKIVDMMKVLSIVDNKKFWQVTAATNTFTNLNSQE 126
Db 66 AVVAYTDQTLSQSNQSVSMDRVTSVLKTMGVLSG-SIITQDTAAATDFTNLNTQK 124
Qy 127 SBAWIFYYKEDAHKTSYYNNILFAIODEETGGVNMATLPIAFDISVIEKEKVLFTIKDT 186
Db 125 DSANYFWGKETSHQNYTNVMFAQNETIGRVNMCPVGPBIRVFTDKRTVLFLITKDY 184
Qy 187 ENYAVTVKAINVQALQSRSDSKVVD--AFKSPPHL 220
Db 185 ANYSYNIQTURFAQPLIDSRLSINDLSEALRSSKYL 221
```

Search completed: June 26, 2005, 16:02:31
 Job time : 164 SECs

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OM protein - protein search, using sw model

Run on: June 26, 2005, 15:56:03 ; Search time 40 Seconds  
(without alignments)  
555.652 Million cell updates/sec

Title: US-10-767-605-2  
Perfect score: 1165  
Sequence: 1 MFFNRVITLTVPSDVNVY.....DAFFSPRHLPRKRHKICNS 231

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing First 45 summaries

Database : PIR\_79:\*

1: Pir1;\*  
2: Pir2;\*  
3: Pir3;\*  
4: Pir4;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	637	54.7	259	2 S32432	toxin cytB - Bacil
2	456	39.1	249	2 A24044	28K crystal protein
3	456	39.1	249	2 B61595	28K parasporal cry
4	103	8.8	477	2 F71918	hypothetical prote
5	101	8.7	477	2 T30838	hypothetical prote
6	99.5	8.5	4540	2 A41874	cytoplasmic dynein
7	96.5	8.3	343	2 A41874	transcription repr
8	95.5	8.2	201	2 A34146	hypothetical prote
9	95.5	8.2	421	1 P64205	thymidine phosphor
10	95.5	8.2	1876	2 E91944	zinc metalloprotei
11	94.5	8.1	249	2 A83963	hypothetical prote
12	94.5	8.1	393	2 S69708	26S proteasome reg
13	92.5	7.9	4688	2 F82885	hypothetical prote
14	89.1	7.8	458	2 E63068	hypothetical prote
15	89.5	7.7	311	2 T32776	hypothetical prote
16	89.5	7.7	1363	2 C84346	hypothetical prote
17	89	7.6	772	1 JQ026	outer layer protein
18	89	7.6	1017	D90550	vsa-like (mycopla
19	89	7.6	1389	2 T41230	hypothetical TPR d
20	89	7.6	1805	1 A61224	hypothetical prote
21	88.5	7.6	717	2 T28247	ORF MSV086 probabl
22	88.5	7.6	735	2 D70174	methyl-accepting C
23	88.5	7.6	1447	2 FB8909	hypothetical prote
24	88	7.6	458	2 B91092	probable invasion
25	88	7.6	458	2 A85938	bacteriophage prot
26	88	7.6	646	2 S60403	probable membrane
27	87.5	7.5	1636	2 S54026	ribosomal protein
28	87	7.5	390	2 T33739	hypothetical prote

## ALIGNMENTS

RESULT 1						
S32432	toxin cytB - <i>Bacillus thuringiensis</i>	C;Species: <i>Bacillus thuringiensis</i>	C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004	C;Accession: S32432; S31476	R;Koni, P.A.; Bilal, D.J.	J. Mol. Biol. 229, 319-327, 1993
		A;Title: Cloning and characterization of a novel <i>Bacillus thuringiensis</i> cytolytic delta				
		A;Reference number: S32432; MUID: 93156045; PMID: 8429550				
		A;Status: Preliminary				
		A;Molecule type: DNA				
		A;Residues: 1-259 <XON>				
		A;Cross-references: UNIPROT:Q04470; EMBL:Z14147; PIDN:CAA78519.1; PID:94930·				
		C;Genetic CS:				
		A;Gene: cytB				
		C;Superfamily: 28K parasporal crystal protein				
RESULT 2						
		Query Match 54.7%; Score 637; DB 2; Length 259;				
		Best Local Similarity 56.0%; Pred. No. 1.2e-41;				
		Matches 126; Conservative 43; Mismatches 54; Indels 2; Gaps 2;				
Qy	7 ITUTVPSSDVNVNYSBIVQAVPOVNQLQNLTKYFGQALGDGSTURFDPKALQJANDLPQA	66				
Db	31 IVLTVESSDLDNENTVYVQPOYINQDLHLLANAFQGIDPLNLFNFEKAQIANGIPNS	90				
Qy	67 AVNTLNQTYQOGTGVSVMDKIVDVKMVLISIVDNKKEFDQVTAAITFTNLSQE	126				
Db	91 AlVKTUNQSVIQQTBEISWVYBQLKCLIQBVQGLVNSTSPNSVEATIKGTFNLQDQI	150				
Qy	127 SEAWIFIYKEDDAHKTSYNNILFAPIDQBDETGGMATLPIAFDISVDEKEKVLPFTKDT	186				
Db	151 DEAWIFHWSLAHTNTSYNNILFSIONEDTGAVMAVPLAPEVSVDYEKQYLVFTKIDS	210				
Qy	187 ENYAVTVTKAINVYQALLOSSRSOSKVDFAK-SPRHLPRKRHKICSN	230				
Db	211 ARYEVKMKALTIVQALHSS-NAPIVDIYNVNNLYHSHNHCITION	254				

N:Alternative names: 28K crystal protein - *Bacillus thuringiensis* plasmids

C;Species: *Bacillus thuringiensis*

C;Date: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 09-Jul-2004

C;Accession: A27520; S06430

R;Bilal, D.J.; Bilal, D.J.

Nucleic Acids Res. 15, 3619, 1987

A;Title: *Bacillus thuringiensis* var. *morrisoni* strain PG14: nucleotide sequence of a gene

A;Reference number: A27520; MUID: 87203386; PMID: 3575104

A;Accession: A27520

A;Molecule type: DNA  
A;Residues: 1-249 <PAA>  
A;Cross-references: UNIPROT:P05069; GB:Y00135; NID:940260; PIDN:CRA68329\_1; PMID:940261  
A;Experimental source: strain morrisoni PG14, 140Kb plasmid  
R;Galjart, N.J.; Sivasubramanian, N.; Federici, B.A.  
Curv. Microbiol. 16, 171-177, 1987  
A;Title: Plasmid location, cloning, and sequence analysis of the gene encoding a 27.3-kilobase plasmid.  
A;Reference number: S06430  
A;Accession: S06430  
A;Molecule type: DNA  
A;Residues: 1-249 <PAA>  
A;Cross-references: EMBL:M35968; NID:g143104; PIDN:AAA22553\_1; PMID:g143105  
C;Genetics:  
A;Genome: plasmid  
C;Superfamily: 28K parasporal crystal protein  
C;Keywords: delta-endotoxin

Query Match 39.1%; Score 456; DB 2; Length 249;  
Best Local Similarity 45.6%; Pred. No. 3.4e-29;  
Matches 99; Conservative 44; Mismatches 64; Indels 10; Gaps 5;

Qy 5 RVITLTVPS-SDVNVNTSEIYQV-AQYVNQDNLTKYFQGAI-----DGSSTLRDFEKA 56  
Db 25 RVITLTVPS-SDVNVNTSEIYQV-AQYVNQDNLTKYFQGAI-----DGSSTLRDFEKA 56  
Qy 57 LQIANDI-POAVVNTLNQTYQQGTVQVSWMIDKIVDMDKNVLSSIVIDNKKFWMDQVTAII 115  
Db 85 LEIANTITPMGAVVSVTDQNVNTQMSVWINKVLEVLKVIGVLSGSVT-DQJTAAV 143  
Qy 116 TNTFTNLNSQESEANLFYKEDAHKTTSYYNNILFADEETGGGMATLPIAFDISVIDIEK 175  
Db 144 TNTFTNLNTQNEANLFWGKETANQNTYTNFLFAIQNAOTGQVNYCVPVGEFEIKVSAVK 203  
Qy 116 TNTFTNLNSQESEANLFYKEDAHKTTSYYNNILFADEETGGGMATLPIAFDISVIDIEK 175  
Db 144 TNTFTNLNTQNEANLFWGKETANQNTYTNFLFAIQNAOTGQVNYCVPVGEFEIKVSAVK 203

RESULT 4  
B64595 hypothetical protein HP0605 - Helicobacter pylori (strain 26695)  
C;Species: Helicobacter pylori  
C;Date: 03-Aug-1997 #sequence\_revision 09-Aug-1997 #text\_change 09-Jul-2004  
C;Accession: B64595  
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.  
Peterson, S.; Lofthouse, B.; Richardson, D.; Dodson, R.; Khaikak, H.G.; Glodek, A.; McKenney  
son, J.D.; Kelley, J.M.; Cottonton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.  
Nature 388, 539-547, 1997  
A;Authors: Wallin, B.; Hayes, W.S.; Borodovsky, M.; Karp, P.D.; Smith, H.O.; Fraser, C.  
A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.  
A;Reference number: A64320; PMID:7394467; PMID:1252185  
A;Accession: B64595  
A;Sequence: nucleic acid sequence not shown; translation not shown  
A;Cross-references: UNIPROT:Q05326; GB:AB000574; PIDN:AAD0767

Query Match 8.8%; Score 103; DB 2; Length 477;  
Best Local Similarity 20.5%; Pred. No. 1.3;  
Matches 47; Conservative 54; Mismatches 90; Indels 38; Gaps 10;

Qy 2 FPFN--RVITLTVPS---SSDVNVNTSEIYQVAPQTVNQALTLAKYFQGAI---DGSSTLRF 51  
Db 199 YPNNLARMIALQKKEQIQTDIRVTKLYDKGLTIDDLQSLKA---QGNLSEYD1LDMQF 256  
Qy 52 DFEKALQIANDIPOQAAVNTLNQTYQQGTVQVSWMIDKIVDMDKNVLSSIVIDNKKFWMDQV 111  
Db 257 ALBQRNLTEYLTNLUVNLKTTT-DAPNQLRERQD-LVSLREQISAIRYQNKQI---- 311  
Qy 112 TAAITNTFTNLNSQSEANLFYKEDAHKTTSYYNNILFADEETGGMMATLPIAFDISV 171  
Db 312 ----NYYPKIDVFPFS-WLFWIQPAPATGRGN-FYPCQONTAQVATLNFDDIGL 362  
Qy 172 DIBEKVLFVTKIDPENYA-----VTVKAINVVA-LQSSRDS 208  
Db 363 SLQKQSIMLGOLANEKLNAYKCLEQKDELYRKSDIARAKIESSKAS 411

A;Molecule type: DNA  
A;Residues: 1-249 <PAA>  
A;Cross-references: UNIPROT:P05069  
A;Note: the authors translated the codon GAA for residue 204 as Gln  
R;Gill, B.S.; Singh, G.J.P.; Horning, J.M.  
Infect. Immun. 55, 1300-1308, 1987  
A;Title: Cell membrane interaction of *Bacillus thuringiensis* subsp. *israelensis* cytolytic  
A;Accession number: A60123; PMID:3570465  
A;Accession: A60123  
A;Molecule type: protein  
A;Residues: 31-41 <GIL>  
A;Note: this amino-terminal sequence was found in both 24K and 25K forms of the purified  
R;Ward, E.S.; Billar, D.J.  
J. Mol. Biol. 191, 1-11, 1986  
A;Title: *Bacillus thuringiensis* var. *israelensis* delta-endotoxin. Nucleotide sequence and  
A;Reference number: A24505; PMID:87086764; PMID:3025452  
A;Accession: A24505  
A;Molecule type: DNA  
A;Residues: 1-249 <PAA>  
R;Ward, E.S.; Billar, D.J.  
J. Mol. Biol. 202, 527-535, 1988  
A;Title: Single amino acid changes in the *Bacillus thuringiensis* var. *israelensis* delta-

F71918 hypothetical protein jhp0552 - Helicobacter pylori (strain J99)  
 C;Species: Helicobacter pylori  
 A;Variety: strain J99  
 C;Accession: F71918  
 R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Nature, 397, 176-180, 1999  
 A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric pathogen  
 A;Reference number: A71800; MUID:99120557; PMID:99233682  
 A;Accession: F71918  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Cross-references: UNIPROT:Q9ZLM7; GB:AE001487; NID:94155086; PIDN:AAD0612  
 A;Experimental source: strain J99  
 C;Genetics:  
 A;Gene: jhp0552

	Query Match	Score 8.7%	Score 101;	DB 2;	Length 477;
	Best Local Similarity	20.1%;	Pred. No. 1.9;		
	Matches 46;	Conservative 55;	Mismatches 90;	Indels 38;	Gaps 10;
Qy	2 PFN--RVIITLTVP---	SSDVNVNTSEIYQVAPQYINQALTLAKYFGQAI---	DGSTLRF	51	
Db	199 YFNNLARMIALQKQLBEIQTDTIKRVTKLVDKGLTIDDLQSKA-	QGNLSEYDILDMQF	256		
Qy	52 DFEKALQIANDIPOQAIVNTLNQTVQGTIVOSVMDKIVNLYLSIVDNKFWMDQV	111			
Db	257 ALEQNQNLTLTLEVNLTKNLKTTIDAPNLQREIRD-LVSREQISALRYQNKQL---	311			
Qy	112 TAAITNTPTLNNSQESEAIIWYKEDAHKTSTYNNILFAIQDEETGGYMATPIAFDISV	171			
Db	312 ---NYPKLDFDS--WLFWIKQPKAYATCRFGN--FYPGQONTAGVTATNIFDDIGL	362			
Qy	172 DIEKERVLFVTIKDTEYA-----VTVKAANVVAQ-LQSSRDS	208			
Db	363 SLQKQSIMLGQLANEKLNAYKLEQEKDEOLYRKSLDIARAKIESSSKAS	411			

RESULT 6

T30838 cytoplasmic dynein heavy chain - Paramaecium tetraurelia  
 C;Species: Paramaecium tetraurelia  
 C;Accession: T30838 #sequence\_revision 22-Oct-1999 #text\_change 09-Jul-2004  
 R;Kandl, K.A.; Forney, J.D.; Asai, D.J.  
 Submitted to the EMBL Data Library, January 1995  
 A;Description: The dynein genes of Paramaecium: the differential expression of axonemal and cytosolic dyneins  
 A;Reference number: Z20502  
 A;Accession: T30838  
 A;Status: preliminary; translated from GB/EMBL/DDRU  
 A;Molecule type: DNA  
 A;Residues: 1-4540 <KAN>  
 A;Cross-references: UNIPROT:Q27171; EMBL:U20449; NID:9987228; PIDN:AAA75449  
 R;Asai, D.J.; Beckwith, S.M.; Kandl, K.A.; Keating, H.H.; Tjandra, H.; Forney, J.D.  
 J. Cell Sci., 107, 839-847, 1994  
 A;Title: The dynein genes of Paramaecium tetraurelia: Sequences adjacent to the catalytic A;Reference number: PC4340; MUID:94334333; PMID:8066840  
 A;Accession: PC4341  
 A;Molecule type: mRNA  
 A;Residues: 1831-2029 <ASA>  
 C;Genetics:  
 A;Genetic code: SCGS  
 A;IntronB: 57/3  
 C;Superfamily: dynein heavy chain, cytosolic

	Query Match	Score 8.5%	Score 99.5;	DB 2;	Length 4540;
	Best Local Similarity	21.6%;	Pred. No. 49;		
	Matches 58;	Conservative 47;	Mismatches 90;	Indels 73;	Gaps 12;
Qy	16 VVNNTSEIYQVAPQ-->YNNQALTLAKYFGQAGDSLRDFEKAQIANDIPOQAQAVNT	71			



Query Match Score 94.5; DB 2; Length 393;  
 Best Local Similarity 24.1%; Pred. No. 4.9;  
 Matches 57; Conservative 42; Mismatches 83; Indels 55; Gaps 16;

Qy 7 ITLTVPESSDVNVYSEIYCOAPVQVNOAQLTLLARYFOGAIIDGSTLRF-----FEKA-LQ 58  
 Db 553 IKALIKDKGDQLYKEV-TVAENNLNATLDKLYQGTLSMVIDGBGBETKEUDQ 611  
 Qy 59 IANDIPQAAYVN----TLNQTYQGTVQVSYMDKIVDI-----MK 95  
 Db 612 IQDLKREIKNIKETSLMNVDAGENTDKSILSEKPTDVSQYLRTVHDNKVTRLAWS 671  
 Qy 96 NVSIVIDNKKEFWDQVTAIAITFTNLNSQBSBAAWIFYKEDAHK-TSYTNILFALIQDB 154  
 Db 672 SYVEVVVDDGKTYKVKAPDLVQRRAADDTLSBEEVYHFEROLPKVNNENELVKDM 731  
 Qy 155 ETGGVMMATPLIAFDI-SVDEIEKVKLVV-----TKTDENAVTV 193  
 Db 732 Q ANPMGEFKLGADLNANVVKPAGKAYMAKERGTLSSEVENHQYTI 776

RESULT 11  
 A83963 hypothetical protein BH2505 [imported] - *Bacillus halodurans* (strain C-125)  
 C;Species: *Bacillus halodurans*  
 C;Accession: A83963  
 R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hirai  
 Nucleic Acids Res. 28, 4317-4331, 2000  
 A;Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and  
 A;Reference number: A83650; PMID:20512582; PMID:11058132  
 A;Accession: A83963  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-249 <stro>  
 A;Cross-references: UNIPROT:Q9K9Y9; GB:AP001515; GB:BA000004; NID:910174886; PIDN:BA062  
 A;Experimental source: strain C-125  
 A;Gene: BH2505  
 C;Superfamily: conserved hypothetical protein yloO; conserved hypothetical protein yloO  
 Query Match Score 94.5%; DB 2; Length 249;  
 Best Local Similarity 21.0%; Pred. No. 2.7%;  
 Matches 37; Conservative 38; Mismatches 64; Indels 37; Gaps 7;

Qy 62 DIPQAAVNTLNQTVQGTVQSVMI-----DKIVDIMKRNVLISIVDNKKEFWDQVTAI 115  
 Db 8 DVGKVPRHNEONGTIMEKGQLVVYADGMGSHQASVSKATELL-KRAMEERAS--- 62

Qy 116 TNTPTNNSQBSBAAWIFYKEDAHK-TSYTNILFALIQDBETGGVMTLPIAFDISDIEK 175  
 Db 63 ---LSPSQSEGMLRNQVHLHNEISLYH---AQHHECOGMGTI---VAAIVDK 109

Qy 176 EKVLFVTKDENTAVTVKAINVQVQALQSSRSKVKUDAF-----KSPRLPLRK 223  
 Db 110 BRVTIAHGDGRAYLINEHGFS-----QKTRDHSLVNLNEVLTGQISDEAEHHPRK 160

RESULT 12  
 S69708 26S proteasome regulatory particle chain RP9N - yeast (*Saccharomyces cerevisiae*)  
 N;Alternative names: protease YDR427w  
 C;Species: *Saccharomyces cerevisiae*  
 C;Date: 22-Aug-1996 #sequence\_revision 06-Sep-1996 #text\_change 09-Jul-2004  
 R;Dietrich, F.S.  
 Submitted to the EMBL Data Library, August 1995  
 A;Description: The sequence of *S. cerevisiae* lambda 3641 and cosmids 9461, 9831, and 941  
 A;Accession number: S69555  
 A;Molecule type: DNA  
 A;Residues: 1-393 <DIE>  
 C;Cross-references: UNIPROT:Q04062; EMBL:U33007; PID:9927685; GSPDB:GN00004  
 A;Gene: SGD:RP9N; RP9; MIPS:YDR427w  
 A;Cross-references: MIPS:YDR427w; SGD:S0002835  
 A;Map position: 4R

RESULT 13  
 F82885 hypothetical protein UU462 [imported] - *Ureaplasma urealyticum*  
 C;Species: *Ureaplasma urealyticum*  
 C;Accession: F82885  
 R;Glass, J.I.; Lefkowitz, B.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.  
 submitted to Genbank, February 2000  
 A;Description: The complete sequence of *Ureaplasma urealyticum*: Alternate views of a mi:  
 A;Reference number: A82870  
 A;Accession: F82885  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-4688 <GLA>  
 A;Cross-references: GB:AE002145; GB:AF222894; NID:96899476; PIDN:AAF30894.1; GSPDB:GN001  
 A;Experimental source: serovar 3; biovar 1  
 C;Genetics:

Query Match Score 92.5%; DB 2; Length 4688;  
 Best Local Similarity 22.3%; Pred. No. 1.9e+02;  
 Matches 44; Conservative 32; Mismatches 72; Indels 49; Gaps 8;

Qy 51 FDFFKALQIANDI-PQAAVNTLNQTVQGTVQSVMDKIV--DIMKVNLSIVDNK 106  
 Db 1509 YDEQRKISLSNNINNPYSKPQTINQNDKSYNIDVNLQVDKQLLANQYLRLLKQLNNDNKT 1568  
 Qy 107 FW-DQV---TAATTTFTNLNSQSSBEAWIIFYKEDAHK-TSYTNILFAIODEETGGVMA 161  
 Db 1569 VWTDPFLNNNAKISFKLSNL-----IHNRAYELEGIYYPDQNSYNDMT 1613  
 Qy 162 TLPPIAFISV---DIEKEKVLFVTKDENTAVTVKAIN-----VQ 200  
 Db 1614 NNQISPNSKHCKPKCIEPEPSLTTNTDNNAKITSAHNAQVHPKLUKTNDBALENDQIVE 1673  
 Qy 201 AL---QSSRDSKVYDA 213  
 Db 1674 AVFAPTNNLNQKVYEA 1690

RESULT 14  
 B65068 hypothetical protein b2852 - *Escherichia coli* (strain K-12)  
 C;Species: *Escherichia coli*  
 C;Date: 12-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 09-Jul-2004  
 C;Accession: B65068  
 R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C  
 A; Rose, D.J.; Mau, B.; Shao, Y.  
 Science 277, 1453-1462, 1997  
 A;Title: The complete genome sequence of *Escherichia coli* K-12.

A; Reference number: A64720 ; MUID:97426617 ; PMID:9278503  
 A; Accession: E6068  
 A; Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A; Molecule type: DNA  
 A; Residues: 1-458 <BLAT>  
 A; Cross-references: UNIPROT:P76639 ; GB:AE000369 ; GB:U00096 ; PID:92367168 ; PIDN: AAC75891.  
 A; Experimental source: strain K-112, substrate MG1655

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Query Match 7.9%; Score 91; DB 2; Length 458;  
 Best Local Similarity 20.3%; Pred. No. 12; Gaps 8;  
 Matches 45; Conservative 37; Mismatches 96; Indels 44;

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Qy  21 IYQVAPQVNQALTLAKYFQGAIDGSTLRFD-----FEKALQIANDIPOQAQAVNTLNQT 75
Db  265 ELYDFPESITRADMIFDRLQNSDQTQTRCYCLAECTMSLA----- 309

```

Qy 76 VQQGTVQSYWMIDKIVDMMKNVLSI-VIDNKXFWDDQVTAATNTFTLNNSQESEAWIFFYY 134
Db 310 -LHGKSELEAAQKAELDVSIDTIVDGK-----ILAIMGLLTGLSGAQKVSHLFE 362

Qy 135 KEDAHRTS---YYNNILFAIQDEEEGQVMATLPIAFDISDIEKEKVLVFTIKOTENYA 190
Db 363 QAKIHSTDIASLYYRVALVPHNEK---IEBARICIDKSQLEPRRRAVVIKECVDDMY 418

Qy 191 VTVKAINVQALQSSRDK---WDAFKSPRHLPPKRHKIC 228
Db 419 VNPNLKNIKYYKEPESESHPVIIIDLKQJTR---IC 456

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RESULT 15  
 T3:2776  
 hypothetical protein D1069.1 - *Caenorhabditis elegans*  
 C;Species: *Caenorhabditis elegans*  
 C;Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004  
 C;Accession: T3:2776  
 R;Murray, J.; Langston, Y.; Clarke, K.; Morris, M.  
 Submitted to the EMBL Data Library, December 1997  
 A;Description: The sequence of *C. elegans* cosmid D1069.  
 A;Reference number: Z21223  
 A;Accession: T3:2776  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 1-311 <MGR>  
 A;Cross-references: UNIPROT:O44789 ; EMBL:AF040641 ; PIDN:AAH94946.1 ; GSPDB:GN000020 ; CBSP:  
 A;Experimental source: strain Bristol N2; Clone D1069  
 C;Genetics:  
 A;Gene: CESP:D1069.1  
 A;Map position: 2  
 A;Introns: 264/3  
 C;Superfamily: *Caenorhabditis elegans* hypothetical protein D1069.1

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Query Match 7.7%; Score 89.5; DB 2; Length 311;  
 Best Local Similarity 21.7%; Pred. No. 9.1; Gaps 6;  
 Matches 36; Conservative 29; Mismatches 60; Indels 41;

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Qy  22 IYQVAPQVNQALTLAKYFQGAIDGSTLRFD-----FEKALQIANDIPOQAQAVNTLNQT 81
Db  138 VIGVRNQYKTSEFSQNKFSKKIDNS--FFEFLISRSQSKIFKILIS-KQKLRKFPF 192

```

Qy 82 QVSVMLDK-----IYDIMKVNLSI-----VIDNKXFWDDQVTT-----AAI 115
Db 193 QVVRPSQSAMLRGGVANVVLDSTQKLQIAQIRSFSIRNTWDEVNSWFTKYSPKAVI 252

Qy 116 TNTFTLNNSQESEAW-----IIFYKEDAHKTSYYNNILFAI 151
Db 253 INFFSDQSAMPNOFWGQYTGKIKKLLFFSBDLDRNPFANILVLI 298